

1 CCGCAACCCC GACGGCGCCC CAAACGGCTGT TGGCGCCGCC GCCCCGCCA  
51 GCCCCGGCTC GCGCTGGTCC CGGTCTCGCC CCGCAGCCCT CGATCTCCCG  
101 TGACTTCCTC GGCCAGGGCG CCTGCGCTC TGGGACCATG TTGCGCTGGC  
151 TGCGGGACTT CGCGCTGCC ACCGCGGCC T GCCAGGACGC GGAGCAGCCG  
201 ACGCGCTACG AGACCCCTT CCAGGCACTG GACCGCAATG GGGACGGAGT  
251 GGTGGACATC GGCAGGCTGC AGGAGGGGCT CAGGAACCTG GGCATCCCTC  
301 TGGGCCAGGA CGCCGAGGAG AAAATTTTA CTACTGGAGA TGTCAACAAA  
351 GATGGGAAGC TGGATTTGA AGAATTTATG AAGTACCTA AAGACCATGA  
401 GAAGAAAATG AAATTGGCAT TTAAGAGTTT AGACAAAAAT AATGATGGAA  
451 AAATTGAGGC TTCAGAAATT GTCCAGTCTC TCCAGACACT GGGTCTGACT  
501 ATTTCTGAAC AACAAAGCAGA GTTGATTCTT CAAAGCATTG ATGTTGATGG  
551 GACAATGACA GTGGACTGGA ATGAATGGAG AGACTACTTC TTATTTAATC  
601 CTGTTACAGA CATTGAGGAA ATTATCCGT TCTGGAAACA TTCTACAGGA  
651 ATTGACATAG GGGATAGCTT AACTATTCCA GATGAATTCA CGGAAGACGA  
701 AAAAAAAATCC GGACAATGGT GGAGGCAGCT TTTGGCAGGA GGCATTGCTG  
751 GTGCTGTCTC TCGAACAAAGC ACTGCCCTT TGGACCGTCT GAAAATCATG  
801 ATGCAGGTTT ACGGTTCAAA ATCAGACAAA ATGAACATAT TTGGTGGCTT  
851 TCGACAGATG GTAAAAGAAG GAGGTATCCG CTCGCTTTGG AGGGAAATG  
901 GTACAAACGT CATCAAATT GCTCCTGAGA CAGCTGTTAA ATTCTGGCA  
951 TATGAACAGT ACAAGAAGTT ACTTACTGAA GAAGGACAAA AAATAGGAAC  
1001 ATTTGAGAGA TTTATTTCTG GTTCCATGGC TGGAGCACT GCACAGACTT  
1051 TTATATATCC AATGGAGGT AATGAAAACCA GGCTGGCTGT AGGCAAAACT  
1101 GGGCAGTACT CTGGAATATA TGATTGTGCC AAGAAGATTT TGAAACATGA  
1151 AGGCTTGGGA GCTTTTACA AAGGCTATGT TCCCAATTAA TTAGGTATCA  
1201 TACCTTATGC AGGCATAGAT CTTGCTGTGT ATGAGCTCTT GAAGTCCTAT  
1251 TGGCTGGATA ATTTGCAAA AGATTCTGT AACCCTGGAG TCATGGTGT  
1301 GCTGGGATGC GGTGCCTTAC CCAGCACCTG TGGTCAGCTG GCCAGCTACC  
1351 CATTGGCTTT GGTGAGAACT CGCATGCAGG CTCAGCCAT GTAGAAGGT  
1401 TCCCCACAGC TGAATATGGT TGGCCTCTT CGACGAATTA TTTCCAAGA  
1451 AGGAATACCA GGACTTTACA GAGGCATCAC CCCAAACTTC ATGAAGGTGC  
1501 TCCCTGCTGT AGGCATCACT TATGTGGTT ATGAAAATAT GAAGCAAAC  
1551 TTAGGAGTAA CCCAGAAATG ATGTTGCATT TTTTGTAA GCCTGATAAT  
1601 TGAAACTTTC AACAATCTCT GGAGTGACTT TTTCTCCTCG AATTGAAAC  
1651 AGTCTATGGC AAAAGAAGCT GCATTTTTT CACAAAAGGG AAGACGGTAA  
1701 CAATGGTCAC TTCAAACATT TGGGCTAAAT TATATGTACA CAGAAATGTT  
1751 CAAAATCATA GTTTTAATGT GTTTTGAAAA GGCCACACAA TTATACCTTAA  
1801 TCTTTCTTA ATAATCCGT AAATCTCTGC CCTGAATCCG AAATCTGAAA  
1851 ATGTAATGGC TTGAACAAAA TTTGTTTGT GTGTTAGAGT TATAATCAT  
1901 TAATCTTTAT TTCGGGTGGT TTACGTTTAT GCCAGTCCCT TTATATTTAA  
1951 ATTTCTTGT T TATATATT TGAATGTCTT TATAGATTTC TTAAATTT  
2001 CTTATAGAAC CTTAAATAGA AAATCATTAC ATTTAAATA TACCTTACAG  
2051 CAAAAGCATC CAAATAAGTA TAGGGTTTAT GTCTTATTT TTCTTCAGC  
2101 TGAATACGAA TGAACACAGT GGTGGAATT T CTGAAGGGAA GTGATGAAAT  
2151 TATATTATT TCACTGGCA CTTTCCATT TTACCACTGT ACCATTATT  
2201 GGTTCTGGA GTTACACT AATTTTCAGT ATTACACTGT TAAATTACCA  
2251 ACACAAGGCA ATTTATTTGA AAGATTCGGT TTATCTGCC ATTGTTTGA  
2301 AAAAGCAGCAG GAAACGAAAT TTTTGACTT GTATCAGCTT CTGCAGAGCA  
2351 TCTTTGTTTT CTTTGTCTT TTGTTCCCTA CCTTTGAAT CAGATTCCGT  
2401 TTTAGTCAGG AAGACTTCTT GGGACCATTC TTAGTAACCT GAAATTTCTT  
2451 TTTTAATTGC ATGAAGTGG A TTGATCATGA GCAAGTGTATG GGCTTTATTT  
2501 CTCCCTCACT GGTGAATATC CTTTGAACCT GCTGTTGCA ATATGGCAG  
2551 CCACAAAGGG GGAGAGATGC CTATTAATC GGCGGGGTGT ATGACTTCTG  
2601 AAAACATTGG ATACCTATT TTGAAAAGGG AAAGGCCAA TTTGGGGAAA  
2651 CATATACCAA TGATGATTCTG (SEQ ID NO:1)

FEATURES:

5'UTR: 1-137  
Start Codon: 138  
Stop Codon: 1569  
3'UTR: 1572

HOMOLOGOUS PROTEINS:

Top BLAST Hits:

		Score	E
CRA 335001098641184	/alt=id=gi 11360341 /def=pir  T50686 peroxis...	927	0.0
CRA 11000479457833	/alt=id=gi 6841066 /def=gb AAF28888.1 AF12330...	834	0.0
CRA 18000005183605	/alt=id=gi 7504235 /def=pir  T22688 hypotheti...	432	e-120
CRA 1000682325160	/alt=id=gi 7499323 /def=pir  T21074 hypothetic...	377	e-103
CRA 89000000196990	/alt=id=gi 7294582 /def=gb AAF49922.1  (AE003...	348	9e-95
CRA 1500000075553401	/alt=id=gi 9758252 /def=dbj BAB08751.1  (AB0...	339	5e-92
CRA 335001098657884	/alt=id=gi 11358611 /def=pir  T49871 peroxis...	330	2e-89
CRA 163000046661776	/alt=id=gi 10176874 /def=dbj BAB10081.1  (AB...	326	4e-88
CRA 105000014652720	/alt=id=gi 10798831 /def=dbj BAB16462.1  (AP...	200	3e-50
CRA 335001098655048	/alt=id=gi 11277065 /def=pir  T47703 Ca-depe...	199	6e-50

BLAST dbEST hits:

gi 10145202	/dataset=dbest /taxon=96...	1108	0.0
gi 1437155	/dataset=dbest /taxon=9606 ...	801	0.0
gi 10333851	/dataset=dbest /taxon=96...	745	0.0
gi 8469752	/dataset=dbest //taxon=960...	363	8e-98
gi 11684041	/dataset=dbest /taxon=96...	307	4e-81

EXPRESSION INFORMATION FOR MODULATORY USE:

Library source:

Expression information from BLAST dbEST hits:

gi 10145202	Placenta Choriocarcinoma
gi 1437155	Retina
gi 10333851	Uterus Leiomyosarcoma
gi 8469752	Breast
gi 11684041	Ovary fibrotheoma

Expression information from PCR-based tissue screening panels:

Leukocyte

1 MLRWLRDFAL PTAACQDAEQ PTRYETLFQA LDRNGDGWD IGEHQEGLRN  
51 LGIPLGQDAE EKIFTTGDN KDGKLDFFEEF MKYLDHEKK MKLAFKSLDK  
101 NNDGKIEASE IVQSLQTLGL TISEQQAEI LQSIDVDGTM TVDWNEWRDY  
151 FLFNPVTDIE EIIRFWKHST GIDIGDSLTI PDEFTEDEKK SGQWRQLLA  
201 GGIAGAVSRT STAPLDRKI MMQVHGSKSD KMNIFGGFRQ MVKEGGIRSL  
251 WRNGNTNVIK IAPETAVKFW AYEQYKKLLT EEGQKIGTFE RFISGSMAGA  
301 TAQTFIYPM E VMKTRLAVGK TGQYSGIYDC AKKILKHEGL GAFYKGYVPN  
351 LLGIIPYAGI DLAVYELLKS YWLDNFAKDS VNPQVMVLLG CGALSSTCGQ  
401 LASYPLALVR TRMQAQAMLE GSPQLNMVGL FRRRIISKEGI PGLYRGITPN  
451 FMKVLPAVGI SYVYENMKQ TLGVTQK (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION  
N-glycosylation site

254-257 NGTN (SEQ ID NO:7)

[2] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE  
Protein kinase C phosphorylation site

Number of matches: 2

1 229-231 SDK  
2 475-477 TQK

[3] PDOC00006 PS00006 CK2\_PHOSPHO\_SITE  
Casein kinase II phosphorylation site

Number of matches: 8

1 22-25 TRYE (SEQ ID NO:8)  
2 65-68 TTGD (SEQ ID NO:9)  
3 121-124 TISE (SEQ ID NO:10)  
4 157-160 TDIE (SEQ ID NO:11)  
5 170-173 TGID (SEQ ID NO:12)  
6 179-182 TIPD (SEQ ID NO:13)  
7 185-188 TEDE (SEQ ID NO:14)  
8 227-230 SKSD (SEQ ID NO:15)

[4] PDOC00008 PS00008 MYRISTYL  
N-myristoylation site

Number of matches: 16

1 52-57 GIPLGQ (SEQ ID NO:16)  
2 119-124 GLTISE (SEQ ID NO:17)  
3 171-176 GIDIGD (SEQ ID NO:18)  
4 201-206 GGIAGA (SEQ ID NO:19)  
5 202-207 GIAGAV (SEQ ID NO:20)  
6 245-250 GGIRSL (SEQ ID NO:21)  
7 253-258 GNGTNV (SEQ ID NO:22)  
8 283-288 GQKIGT (SEQ ID NO:23)  
9 295-300 GSMAGA (SEQ ID NO:24)  
10 322-327 GQYSGI (SEQ ID NO:25)  
11 326-331 GIYDCA (SEQ ID NO:26)  
12 359-364 GIDLAV (SEQ ID NO:27)  
13 392-397 GALSST (SEQ ID NO:28)  
14 399-404 GQLASY (SEQ ID NO:29)

15 442-447 GLYRG (SEQ ID NO:30)  
16 446-451 GITPNF (SEQ ID NO:31)

[5] PDOC00018 PS00018 EF\_HAND  
EF-hand calcium-binding domain

Number of matches: 3

1 32-44 DRNGDGWDIGEL (SEQ ID NO:32)  
2 68-80 DVNKDGKLDFEF (SEQ ID NO:33)  
3 99-111 DKNNDGKIEASEI (SEQ ID NO:34)

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	292	312	1.053	Certain
2	345	365	0.613	Putative
3	381	401	1.544	Certain
4	446	466	0.733	Putative

BLAST Alignment to Top Hit:

>CRA|335001098641184 /alt=id=gi|11360341 /def=pir||T50686 peroxisomal  
Ca-dependent solute carrier [imported] - rabbit  
/org=rabbit /taxon=9986 /dataset=nraa /length=475  
Length = 475

Score = 927 bits (2371), Expect = 0.0

Identities = 454/477 (95%), Positives = 466/477 (97%), Gaps = 2/477 (0%)

Query: 1 MLRWLRDFALPTAACQDAEQPTRYETLFQALDRNGDWDIGELQEGLRNLGIPLGQDAE 60  
MLRWLR F LPTAACQ AE PTRYETLFQALDRNGDWDI ELQEGL+LGIPLGQDAE  
Sbjct: 1 MLRWLRGVLPPTAACQGAEPPTRYETLFQALDRNGDWDIRELQEGLKSLGIPLGQDAE 60

Query: 61 EKIFTTGDNKDGKLDFEERMKYLDHEKKMKAFLKSLDKNNDGKIEASEIVQLQTLGL 120  
EKIFTTGDNKDGKLDFEERMKYLDHEKKMKAFLKSLDKNNDGKIEASEIVQLQTLGL  
Sbjct: 61 EKIFTTGDNKDGKLDFEERMKYLDHEKKMKAFLKSLDKNNDGKIEASEIVQLQTLGL 120

Query: 121 TISEQQAELILQSIDVDGTMVDWNEWRDYFLNPVTDIEEIRFWKHSTGIDIGDSLTI 180  
TISEQQAELILQSID DGTMTVDWNEWRDYFLNPV DIEEIRFWKHSTGIDIGDSLTI  
Sbjct: 121 TISEQQAELILQSIDADGTMVDWNEWRDYFLNPVADIEEIRFWKHSTGIDIGDSLTI 180

Query: 181 PDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQ 240  
PDEFTE+E+KSGQWWRQLLAGGIAGAVSRTSTAPLDRLK+MMQVHGSKS MNIFGGFRQ  
Sbjct: 181 PDEFTEERKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKMMQVHGSKS--MNIFGGFRQ 238

Query: 241 MVKEGGIRSLWRGNNTNVKIAPIETAVKFWYEQYKLLLTEEGQKIGTFERFISGSMAGA 300  
M+KEGG+RSLWRGNNTNVKIAPIETAVKFW YEQYKLLLTEEGQKIGTFERFISGSMAGA  
Sbjct: 239 MIKEGGVRSLWRGNNTNVKIAPIETAVKFWYEQYKLLLTEEGQKIGTFERFISGSMAGA 298

Query: 301 TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGVPNLLGIIPYAGI 360  
TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILK+EG GAFYKGVPNLLGIIPYAGI  
Sbjct: 299 TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKYEFGAFYKGVPNLLGIIPYAGI 358

Query: 361 DLAVYELLKSYWLDNFAKDSVNPGVMLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE 420  
DLAVYELLKS+WLDNFAKDSVNPGV+VLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE  
Sbjct: 359 DLAVYELLKSHLDNFAKDSVNPGVVLGGCGALSSTCGQLASYPLALVRTRMQAQAMLE 418

FIGURE 2B

Query: 421 GSPQLNMVGLFRRISKEGIPGLYRGITPNFMKVLPAVGISYVYENMKQTLGVTQK 477. (residues 1-477 of SEQ ID NO:2)

G+PQLNMVGLFRRISKEG+PGLYRGITPNFMKVLPAVGISYVYENMKQTLGVTQK

Sbjct: 419 GAPQLNMVGLFRRISKEGLPGLYRGITPNFMKVLPAVGISYVYENMKQTLGVTQK 475  
(SEQ ID NO:4)

>CRA|11000479457833 /alt=id=gi|6841066 /def=gb|AAF28888.1|AF123303\_1  
(AF123303) calcium-binding transporter [Homo sapiens]  
/org=Homo sapiens /taxon=9606 /dataset=nraa /length=411  
Length = 411

Score = 834 bits (2132), Expect = 0.0

Identities = 409/410 (99%), Positives = 409/410 (99%)

Query: 8 FALPTAACQDAEQPTRYETLFQALDRNGDWDIGELQEGLRNLGIPLGQDAEEKIFTTG 67

F LPTAACQDAEQPTRYETLFQALDRNGDWDIGELQEGLRNLGIPLGQDAEEKIFTTG

Sbjct: 1 FVLPPTAACQDAEQPTRYETLFQALDRNGDWDIGELQEGLRNLGIPLGQDAEEKIFTTG 60

Query: 68 DVNKDGKLDFEERMKYLKDHEKKMFLAKFSLDKNNDGKIEASEIVQLQTLGLTISEQQA 127

DVNKGDKLDFEERMKYLKDHEKKMFLAKFSLDKNNDGKIEASEIVQLQTLGLTISEQQA

Sbjct: 61 DVNKDGKLDFEERMKYLKDHEKKMFLAKFSLDKNNDGKIEASEIVQLQTLGLTISEQQA 120

Query: 128 ELILQSIDVDGTMVDNEWRDYFLFNPVTDIEEIIIRFWKHSTGIDIGDSLTIIPDEFTED 187

ELILQSIDVDGTMVDNEWRDYFLFNPVTDIEEIIIRFWKHSTGIDIGDSLTIIPDEFTED

Sbjct: 121 ELILQSIDVDGTMVDNEWRDYFLFNPVTDIEEIIIRFWKHSTGIDIGDSLTIIPDEFTED 180

Query: 188 EKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGI 247

EKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGI

Sbjct: 181 EKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGI 240

Query: 248 RSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIY 307

RSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIY

Sbjct: 241 RSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIY 300

Query: 308 PMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGVPNLLGIIPYAGIDLAVYEL 367

PMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGVPNLLGIIPYAGIDLAVYEL

Sbjct: 301 PMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGVPNLLGIIPYAGIDLAVYEL 360

Query: 368 LKSYWLDNFAKDSVNPVMVLLGCGALSSTCGQLASYPLALVRTRMQAQA 417 (residues 8-417 of SEQ ID NO:2)

LKSYWLDNFAKDSVNPVMVLLGCGALSSTCGQLASYPLALVRTRMQAQA

Sbjct: 361 LKSYWLDNFAKDSVNPVMVLLGCGALSSTCGQLASYPLALVRTRMQAQA 410

(SEQ ID NO:5).

Score = 80.0 bits (194), Expect = 6e-14

Identities = 80/388 (20%), Positives = 156/388 (39%), Gaps = 59/388 (15%)

Query: 95 FKSLDKNNDGKIEASEIVQLQTLGLTISEQQAELILQSIDV--DGTMTVDNEWRDYFL 152

F+L+H+ DG ++ E+ + L+ LG+ + + E I + DV DG +

Sbjct: 21 FQALDRNGDWDIGELQEGLRNLGIPLGQDAEEKIFTTGVDVNKGK----- 68

Query: 153 FNPVTDIEEIIIRFWKHSTGIDIGDSLTIIPDEFTED EKKSGQWWRQLLAGGIAGAVSRTST 212

D EE ++ K + EKK + + L + +

Sbjct: 69 -----DFEEERMKYL-----DHEKKMFLAKFSLDKNNDGKIEASEIV 105

Query: 213 APLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAY 272

L L + + ++ + I V R + N I E ++ FW +

Sbjct: 106 QSLQTLGLTISEQQAELILQSIDVDGTMVDNEWRDYFLFNPVTDI---EEIIRFWKH 161

Query: 273 EQYKKL-----LTEEGQKIGTFER-FISGSMAGATAQTFIYPMEVMKTRLAV-GKT 321  
 + . . . . . TE+ +K G + R +G +AGA +T P+ +K + V G  
 Sbjct: 162 STGIDIGDSLTIPEFTEDEKSGQWRQLLAGGIAGAVSRTSTAPLDRKIMMQVHGSK 221

Query: 322 GQYSGIYDCAKKILKHEGLGAFYKGVPNLLGIIPYAGIDLAVYELLKSYWLDNFAKDSV 381  
 I+ . + + +K G+ + +G N+ I P+ + YE K . . . . +  
 Sbjct: 222 SDKMNIFGGFRQMVKEGGIRSLWRQNGTIVKIAPEAVKFWAYEQYKKL---LTEEGQ 277

Query: 382 NPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMGLFRRIISKEGIP 441  
 G . . . . G++ . . Q . YP+ . + +TR+ . At+ . . . + . + +I+ . EG+  
 Sbjct: 278 KIGTFERFISGSMAGATAQTFIYPMEVMKTRL---AVGKTGQYSGIYDCAKKILKHEGLG 334

Query: 442 GLYRGITPNFMKVLPAGISYVYENMK 469 (residues 95-469 of SEQ ID NO:2)  
 Y+G PN + +P GI . VYE +K  
 Sbjct: 335 AFYKGVPNLLGIIPYAGIDLAVYELLK 362 (SEQ ID NO:6)

Hmmr search results (Pfam):

Model	Description	Score	E-value	N
PF00153	Mitochondrial carrier proteins	305.4	3e-88	1
PF00036	EF hand	50.7	1.7e-12	3
PF00404	Dockerin domain type I	9.7	0.26	1
PF01978	Protein of unknown function	2.7	9.5	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00036	1/3	27	51	5	29	18.7	0.002
PF00404	1/1	67	85	1	22	9.7	0.26
PF00036	2/3	61	87	3	29	19.7	0.001
PF00036	3/3	90	118	1	29	17.2	0.0051
PF01978	1/1	110	121	1	13	2.7	9.5
PF00153	1/1	193	472	1	313	305.4	3e-88

1 AACCATGTT AGTGTGCA GTCTGCTGGCA CACACATGCA GTTGTGTAAC  
 51 CACTACCACC AAAAGCAAGA TGTAATAG CTCCATCACC CCCACAAGCC  
 101 TTCTGATGCT CTTTGTCTAT CAATTCCTT CCCGCTAGTC ACAACTGGTA  
 151 ACTACTGATT TGTGTTCTGT CCCTATAGTT TTGCTTTTC CAGAATGTCA  
 201 TTGTTGACAG GTATCAGTAA TTCATTCTT TTATTGCTA ATTACTATCT  
 251 CACTGTATGA ATGCAACACA GGTTGTTTAC CAGTTCACCC GTAAAGAAC  
 301 ATTTTGTTC TGCGCTTGAC AGTTATGAAT AGAACTGCTA TAAACCCCTA  
 351 AGTAAAAGTT TTGGTGTGAA GATAATTTC TCAGCAAAAA CGCTGACAGG  
 401 TAATTTTCT AAGTATTACT TTTTTAAAAA AGTAAAATAG CCTGTAGCCC  
 451 CAGCTACTCA GGAGGCTGAG GCAGGAGAAT AGCTTGAAAC CAGGAGGCGG  
 501 AGGTGCACT GAGTTGAGAT TGTGCCACTG CATTCCAGCC TGGGCGACAG  
 551 AGCTAGACTG TCTCAAAGAA AAAAAAAA AATAACAAAT AAATAAAAAG  
 601 TAAAATGAAA GCATGTAAGT GTAAGATGAC TAGTTCAAGC AACCTCTTT  
 651 CAAGTACAGA GTATTTCAGAG TAGAGATTA AAGAGGTTT CAAGGACAGA  
 701 GAAAATTGAG AGTTTGAAGG CAGTTCCAAA GGAAGGCAAT GATTCTTAAT  
 751 AAGACTGGAA GTTGGAAAGTA ATATAAAAAG ATAAAATCAGT TTCAAGATGA  
 801 TTTTACTAAG CAGGCAGCCC TTAATTTACA AATTCTAGAT TCATACATAT  
 851 CTTAAACATA CAAAATGATA TGAGGAGAGG TAAGTTCAAGG GTCTGAGTT  
 901 CTGGCTGTTG TTGGAACTGA TTTCTGTGTA GTGATTCAAGA AGATGTGAGA  
 951 CACCCCTAATT TACAAGTACA GAGGTATCTT CTTTCTGCA AACAGCAGTA  
 1001 CAACAATAGT TCCCTTACG CAGCTGTGAA TGAACAGGAT TATTACAATT  
 1051 AATGATATCT CATTGATTG GCGCCTTACA GAATTAAGAC CTTTCACACC  
 1101 TAATATACAA CTTTGTGTG AAGGCAGATA TTTATATTCT CATTTTACTG  
 1151 ATGAGAGACT ACCCGGAGAC GCTATGTCAC ACCTGAAGGA TTAGTACTT  
 1201 TCTCTGTTAA GTCCAATGTT CCTTCCGTTA TTCCATGCTA GGCAGTAATA  
 1251 AGTTCTGTCT TGCCCTGAGTA ATAAGCTCCA AACCTCGGAA CTGCACCCAT  
 1301 CTTGAGAAGG AGGAGGGCGC TGTGGTTTT TCTGATAAGT GCAGCTGGCA  
 1351 GACACTCTAT ACGCTTAATC ACGGGCAAAT CCTACCTAAG CTGCCTACCA  
 1401 AACTAGTCCT TCTTTTCCCC GTTGCCCCACG CAGATGGCTG TTGATCTTTT  
 1451 CTGCAACAAA TCCAGGAGTT TCTCTTTTTT GTTTTATAAT TGCTCCAATA  
 1501 GATGCTTTAG GATTTAACCTC TCTGCTTTTTT AAAGCAGAAT CGCCATCCCA  
 1551 GGTGTGCAAC CACGAAAAAA TTAGACATCC GTGAGAGACA ATGCCCTCCA  
 1601 TGGCCCAGTT TCCAGGCAGA GAGAAGCAGC TCTGGGCTGA CCGCCAAGGC  
 1651 TCCGGCCCGA GAGGGTCTTT AAGTGGAGTA ACCAGTCTTC AAGACCCCGC  
 1701 TCCAAGCCA CCGACGGCT GACGCTGCAG CCCTGGACCT GCTGGGGGCC  
 1751 TCTTCCTCGG ACCCGCATGC TGACAGCGGG ACTGGCAACT GGGCAGAGGT  
 1801 CGACCCCGGG TCCGCACAGC ACCTCCCGAG ACCCAGCTCC CAGCTCCCTC  
 1851 ACTTCCGGCT CTCTGGAGGC GGGCCCGGCC AGTGCCGGCG AGGCCAGCGC  
 1901 GGGGAGCTCC TCCCCAGCAG CGGGGGGACG GCCACACCCCT GCGCGCCCGC  
 1951 CGGGCTCGGG TGGGGTCTCC GCTCTGCGC CCTGCGCGCC GCAGCCGCAC  
 2001 CCCCGACGGC GCCCCAAACG CTGTTGCGCC GCGCGCCCCG CCCAGCCCCG  
 2051 CCTCGCGCTG GTCCCGGTCT CGCCCCGCGAG CCCTCGATCT CCCGTGACTT  
 2101 CCTCGGGCAG GCGGCTGCG CCTCTGGGAC CATGTTGCGC TGGCTGCGGG  
 2151 ACTTCGTGCT GCCCACCGCG GCCTGCCAGG ACAGGGAGCA GCCGACCGCG  
 2201 TAGGAGACCC TCTTCCAGGC ACTGGACCGC AATGGGGACG GAGTGGTGG  
 2251 CATCGGGCAG CTGCAGGAGG GGCTCAGGAA CCTGGGCATC CCTCTGGGCC  
 2301 AGGACGCCGA GGAGGTGGGT CGCCGCCGGG GCGCCGCCGT AGCGTAGGGA  
 2351 GGGCTCGGGG CGCTGGGAC ACTGCGAGGA CCGAGGAGGG CGGGGGCTTG  
 2401 AGGCCTGCCCC AGGAGAGGAA GGAGGAACCTG TGGGCCAG CGCTCCGGTG  
 2451 GCTTCAGAAA CTCGGCGTG GGGCCGCGAC CGGGCACCCCC GGTACACAGAA  
 2501 GTGGGTCTATA ATACGAAAGT CTACTGGTAT TTGTCAGAT AAAATGAGTG  
 2551 TTGTTGACAC TCTGGCCAC GGGCACTGTT AAATTTTAA GACACTTTTG  
 2601 TCCTGAATCC ATCCCAGTT CTTTGTGTTT TGTTTAAATA CCTTGCAAGAC  
 2651 ATGTAATCCG TTTTAGCTGT CAGACTTCAG TGGGTCCCAA GTTTGTATA  
 2701 AAGGCGCACA CATTGATCT CTTTCAAGC TGCTTGTAA CAGCAGCTAT  
 2751 GTGTATTGTC TACTGTTGA AAAACTGTTTG AAAACCAATC GCGTGTGTTCC  
 2801 CCCACTTCCT GTTGGAGAAGG AATGGCGGCC TTCCATTGTT TAAGACATT  
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2901 TGGCACTGAG CAATTTCAATT TTCTCTGAGT CATCTTAACCT GTGCCCTG  
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 58801 ACAGCTTTT TTAAGCATCT TAATATGATT GTTTATATTA CTCCACACAC  
 58851 CTCTAAAAA AACTTAATAC CCTATTTTC CTCTCATATC CTCCCATATC  
 58901 AGTTAATAGT ATCACCTTC CAACTCCCCA CTGCCCCATC CTGTGTTCA  
 58951 AGCTAGAAGT ATGGGGTTA TCCTTATAC TACCATTTCC CTCACCTTCC  
 59001 AGATGCAGGT GGTCAACAGT CAGTTTTGTT AAGACATCAA TAGATTATCT  
 59051 TGCTTCCATT TCCCTGGTCA CTTCCCTCAT CAGATCCTCC TTGCACTAA  
 59101 CGGGTCTCTC TGGCTTGGT CTTAGCCCCA CAATAGAGGT AATACATGAA  
 59151 AGAGAATGTA TCAACAAATT GTACAGTCTT TTGAGTGACA ATATGTGCTA  
 59201 GGTATTTGTT CCATGTAAAA TTACTTCATT TGAATCCCAT GATGATAGAG  
 59251 TTAATATGAA CAATCATATT TTGTTTTTT TTATATCCAG GTTATGAAAA  
 59301 CCAGGCTGGC TGTAGGCAAA ACTGGGGCAGT ACTCTGGAAAT ATATGATTGT  
 59351 GCCAAGAAGA TTTTGAACAA TGAAGGCTTG GGAGCTTTT ACAAAGGCTA  
 59401 TGTTCCAAT TTATTAGTA TCATACCTTA TGCAAGGCTA GATCTTGCTG  
 59451 TGTATGAGGT GAGTTTGAG AAATCTTTG AATTGGAAAA TGCACTTGA  
 59501 TCTTGTAGA ATTGGACTTT ATATGAAGAA GTAGATATAT ACCAGAAAAC  
 59551 AGTGTGTGAC CAGAAGTAAA TTCAAGCATG TGTTATTTGA ACTTTCAAGT  
 59601 AACTTGAGTG TGAATATGCA TGGGTCACT TTGTTATTAG ATTTCTTGG  
 59651 GAATTGCTTT TGTTAATGAA GAGTAGACTC AAAGTTAGGT ATAGTTGTT  
 59701 ACCTAAAAG GTGTTCTAG AGATTTTTTC CTTTGTTTG GATTGCAAA  
 59751 AATCTGACAT TAAGCCAAGT GACTAATGTG ACTAACATGA GTAATACAGT  
 59801 TTCACTCCCT GTACGGAAGA ATACAAATCT TGGATCAACC CTGCAATCTA  
 59851 AATCATTTAA TAATTTATGA ATCTCACAAA CAATTATTGA GCACACACTA  
 59901 TACAAACCAC TAGGTTAGAC ACTGGATCTG GGGATTCAAA GGACTCAATG  
 59951 TGTCCTTGA AGAAACTGAA GGTCTGGTGG GGGAGACAAA CGACTAAAAC  
 60001 TCAGCGTGGT TATCTGTGCT GCGACAGACA TGAGCCAGGG TGATGTTAG  
 60051 GATGAGACCT AAGCTACAGC GTAGAGGAAG AGTGGAAATGT GTAATGAAAA  
 60101 GAAGAGTCGA ATTTCCTTT TAAAGAGCTT TATTGAGATT TAGTTCATAT  
 60151 TCCTTACATT TCACTCATTT GAAGTGTACA AGCAAATGGT TTTGGCTTC  
 60201 TTACATAATT TTTAAAATT ATTATAAAAT ATAAAATTTG CCATTTACT  
 60251 AATTTAAGT GTACAATTCA GTGGCATTAA TTACATTCCAC AATATTGTGC  
 60301 AACCATCAAC ACTATTTCA AATCTTTTC CTCACCTCAA ACAGAAACAC  
 60351 CTTAACCTTT AAGCAATAAC TTCCTACCC CCGTAACCTCA AACCTTTGGT  
 60401 AACCTCTAAT CTGCTTTCTA TGTCTAGGAA TTACCCATT CAAGATATCT  
 60451 TATAAGTGA ATCATACTAGT ATTTCCTTT TTGTTGCTGA TTTATTACTC  
 60501 TTAGCATAAT GTCTCTAAGG TTTGTTCATG TTGTTGCTAG TATCAGAACT  
 60551 TCATTTCTT TCATGGCTGA GTAATATTCC GTTATGTGTA TATACCACTAT  
 60601 TTTGTTTAGT CTTTCATCTG TTGAAGAGCA TTGTTGATTAT TTCTACTTTT  
 60651 CCAACATTGT GAATAATGCT GCAGTGAACA TTGGCATCTG CGTATCTGTT  
 60701 CGAGTCTATG CTTTCATTC CTTGGGTAT ATATCTAGA ATGGAATTGC  
 60751 TGAGCCATAT GGTCAATTG TGTTAGCTT TTAGGAACTA TGAGACTGTT  
 60801 TTCCATAGTG GCTGCACTTA CATTCTCACC AGCAACATAC AAAGTTCCA  
 60851 GTTTTCCAC GTCTTATTA ACACCTAATT TCCATTTAA AAAAGCTTAT

60901 TTTTATTATG GCGTCCTCT TAGGTGTGAG GTGGTATGGT TCAGGACTTT  
60951 ACTTCTTGTG CTGAGTTTT TAAAAAAATTG TGATTAACAT CACATAACAT  
61001 AAAGTTTATG ATTTAACCA TTTTAAATA TATAGTACAG TAAGTGTAA  
61051 CTGTTTGTGG TTGTTGTGC AACAGATCTC TAGAACTTT TCACCTCTCA  
61101 AAACCTAACAC TCTATAGTC TTAAACAACA GCTCCCAATT TCCCCTCAC  
61151 CCCAGCGCTG TGAAACCTAC TTTCGTTTG TATGAGTTG ACTACATTAA  
61201 ATACCTTGTG TAAGTGAAT CATGTGGTAT TTCTCTTCC GTGACTGGCT  
61251 TATTTCATGT AACATAGTT CCTCATGATT CATCCATATG ATAGCATA  
61301 ACAGGACTTT TTGTTTTTA AGGCTGAATA ATAATTTGTT GGGTATATAT  
61351 ATCACATTTC TTATTTCAT CTGTTGATGG ACATTTGGAT TGTTCTACA  
61401 TCTTGAATAT TGTGAATAGT GCTGCAGTGA ACATGGTTGT GCAAATATCT  
61451 CTTCAGATA CTGTTTCAAG TTCTTTTGAA CATAACTCA GAAGTGGAA  
61501 TTCTGGGTCA AATGGTAATT CTATTTTAA GTTTTGAGG AACCTCCATG  
61551 TCATTTCCA TAGTAACTAG ACCTTTTGT TTTTTAACAT TTCTATCAAT  
61601 GTACACCAAG ATTCAATTT CTCCATGTCC TCCCCAACAC CATTAAAGTGG  
61651 GGTGGTGGTC TACTACTATT GCTGTGTTGC TGTTTATTCC TCCCTTCAGT  
61701 TCTGTAAGTG TTGCTTCAT ATATTTAGGA GCTTAATATT AGGTCATAT  
61751 GAAGTTATAA TTCTTCCTG GTAAAGTGCAC CCATTTATCA TTATGTAATG  
61801 TCCATTTTG TCTCTTGTGA CAGTTTGTGT CTTAAATCT ATTTTGTCTG  
61851 ATGTAATTAT GGCCACCCCT TTCTCTTTG GTGTCCT TAGATCTAAA  
61901 ATCTTTTCC ATCCCTTCAC TTTCAGCTTA TGTTGTCCT TAGATCTAAA  
61951 GTGAGTCTCA TAGATAAGGT ATAGTTGATT CTGTATGTGT TATTCACTCA  
62001 GCAATTATAA TCTTTAGTT AGGGGATTAA ATCCATTTCAC ATTTAAAGCA  
62051 GTTACTGATA GGGAAAGGACT TACTGTGTC ATTTGGCTAG CTACCTTTT  
62101 ATCTTGTCC TGTTGGTTTT CTGTTTTTCC CTTCCTCTC TCCTGGCTTC  
62151 TTCTGTGTT TGTTGATTT TTTTTTTTG GTAGTGATAT GTTCTGATT  
62201 CCTTCTCATT TCCCTTTGTG TGCAATTCTAT AGATGCTATT TTGTTGGTTA  
62251 CCATTGCAAC TACATAAAGC ATACTAAAGT TATAGCAACT TATTTAAAGC  
62301 TGTTTACAAC TTAACTTCAG TGGTATATAA AACTCTATTT CTTTACATAT  
62351 TTCACCTCT CCCCCACAAAC TTTATGTCTT TTGATATTGT ATATCCTTAA  
62401 CATAGATTAA TAGTTACTTT TTATGTTTT CTTCCTTAA TTCTGTTTAA  
62451 ATTTTGTTT TGAAATTAG ATTTCAAGT TATTTATATA CCTTCATTAC  
62501 AATACTATAG GATTTTATAA TATTCTAAAT ATTGACCTTT ACCATAGAGT  
62551 TTCAATTTTG GTGGTTTGTG GTTGCTATT ATCATCCTTT TGTTCTCCT  
62601 TTAGCCTTT CTTGTAGGGC CGGTCTAGTG GTGATAAGCT GTATCAGCTT  
62651 TTGTTTGTCA GGGACAGTCT TAATTTCTCC TTTTTGAAG GGCAGTTTG  
62701 CCCATACAGT ATTTTGTG GGCAGTTTT TTAAGTTTCA AAACATAGAA  
62751 TATAACATTC CATTTCCTC TAACCTGCAA GATTTCCATT GAGAAATGCA  
62801 CTCATGGAT TTTTAATCC ATTGAGATAA TTTTTAAATC CTGAGGATT  
62851 TAAAATTTT AGTCTTACAG GATTAACAAAAA TTAAAAAGTT AAACCTGTTA  
62901 TATAACATAT TAACATGTAT TTTATACTTA AAGTATCTTA TGTTAAAAAA  
62951 GTGATTATC ATATATATTT TATACAGTTT CTCTTAATTA TTGCTTCTA  
63001 ATGAAATACA GGGACCTAGA GTAACAGGGAA TAAAGTATGG CCTTTGATC  
63051 AGCACGCCCTG GTTCTGAGTC CTTCTTAAAAA AAACCTGGG CCTGGTGTGG  
63101 TGGCTCATGC CTATAATCTC AGCACTTGG GAGGCCGAGG CGGGCGGATC  
63151 ACCTGAGGTC AGGAGTTGA GATCAGCCTT GCCAGCATGG TGAAACCTG  
63201 TCTCTACTAA CAGTACAAAG ATTAGCTGGG CGTGGTGGTG GGTGCTGTG  
63251 ATCCAAGCTA CTCAGGAGGC TGAGGCAGAA GAATCGTTG AACCTGGGAG  
63301 GCAGAGATTG GGCCACTGCA CTACAGCCTG GGTGACAAGA GCGAGACTCC  
63351 ATCTCAAAAA AACAAACAAA AACTCCGCTG AGATGAATT TTCTCATTT  
63401 TAAAATCAGA ATAATAGATT TATGTAAGAG TTCTGTAAAG GCTCAAATGA  
63451 AATATATGTA ACGTGTAAAA TGAGATACAA TTAGTAGAAT TATATTATTT  
63501 TATTAATACT CACCATAAGA GGTGTTCTT AGATCCTGCA GCGTTGCTG  
63551 CGCAGTTCAC GTTTGTTAG AAGAATGTCA GTAAACGGTG CAAACCTCAT  
63601 GTGTTCCGCA CCCCCAGTGG CCTCCCACCT CTCCACAGAG TCACCGCTC  
63651 CTGAGTGTGCC TGCTGTTCT GCAAATGCGT GGCCTCATCC TGCAGAAACG  
63701 GGGCTCTCA TGAGGTTGAG AATAGCTGTG AAAATGTTA CGTTGAAGTT  
63751 GTAGAGTTCG TTAATTATTT TCTCTTTAT TTCTCTGGCA GCTCTTGAAG

63801 TCCTATTGGC TGGATAATTT TGCAAAAGAT TCTGTAAACC CTGGAGTCAT  
63851 GGTGTTGCTG GGATGCGGTG CCTTATCCAG CACCTGTGGT CAGCTGGCA  
63901 GCTACCCATT GGCTTTGGTG AGAACTCGCA TGCAAGCTCA AGGTGAATT  
63951 TTGATTACAG AACCACACCG ATAAAAGTGC TGCAACCAGTA ATGTGCTTT  
64001 AGAACTCCAA GTTCTACTAA GATGCAGACT GTAGTTTAA GACAGTATT  
64051 CTCACACCTT TTTTCATTAT TGCCCTCTTA AGGAATCTT TCAGAAATT  
64101 TTTTCTAAA TGCTCCCTCG TCATGAAATT TTAATGCGAC AGAAGCATTG  
64151 CATACTGACT GTATGCATAC ATATGCCTTA TAGATAAAACA GAGTACTATT  
64201 TTTTTGACT GTGTTACATG CACGTTTAA GATTATAAGC TTTAGTATCT  
64251 GATGGATTG GGTTCAGATC CTTGCCCTAG ACTTCTTGGG GTTTTAATG  
64301 GGAATGAAAA TTGTACAGTG TTGTAAGAAT TACCAACAAT ATAAATAAAG  
64351 CACTTGGGT TTGTTAAATT TTTGGTAAAT GGTGGTTGGA ATCATT  
64401 AGTGTGCGT AGACCCCTACA AGTTTGAGC TGTGATTCT CCTCACTGTG  
64451 ACACGTCTC CATTGTTGGC TTTGATTACA CTGTACCATC CTGGTTGTC  
64501 TGCCAGCCCA TTGATAACTT TTACCATTTG CTGGCTTTA TTGCTATCCC  
64551 CACTCTATTAA AAGTATGCAT TCAAATGCCT TTCTTTCTC TTTGATGCTT  
64601 TCCCTGGTCA GTCTTATCCA TTGTTTCTT AAGTAGTACA CCTTGGGAT  
64651 CTACAGCTCT ATTCCCAACC TCCCTTCCAA GTGCCAGCCA CAGCAACCCC  
64701 AGCCAAGCAG TCAGTAACTA ATTGGCAAAT ACTCCCTGAG CCATTGTC  
64751 ATTCTAGACA CTGCCAGATG CTAGGGTAG AGCAGTCAAC AAGTCAGGTG  
64801 TGGCCCCCGCC AGTGTAGAGT AGAGAAAGACG TTATGTCAG CAAGTAAACA  
64851 ACCTGGTTAA ACCAACTCTT CTTTGTAG GGGAGCACAG AGCAAGGAGC  
64901 TATAACCTAA CTTGGCGCT GCAGAATGCT GTCACTGAAG CTGAGACTGG  
64951 AAAGATGAGT GGGAGTTAGC TGGGCACAGG CCAGTGGAGT GGGAAACAGAA  
65001 AACATTCCAG TTGAGGGAAA GCATGTGTGA AGACACTGAG GCAGGCACCA  
65051 ACATGGTGTAA TTAAAGGAGC TGAGAGACAG TCATGGCTGT AGAGAAAAAC  
65101 ACAAAAGTAGT GAACTACAG TTTCTTGTGT ATTCTCTCAT TTCACCATCA  
65151 TAACCATCTT GGGGATGGGA ATACTAACAT TATCCCCATT TTTCAGATGA  
65201 GCAACTGGGG CAGAGAGAAT TTAAGTAAC CCCACAAGAT TATACTGTG  
65251 GTAAATAGTG GGAAGTAAAT TCAGACACAT GCAGTCTGAT TCTAACCTC  
65301 CTGCTGCCA GCTCTGATCC AGAACTTTGC ATGACTGATA CGGCTGATAG  
65351 ATTGCTATG GCTGATAGAC TGTCTTTCT GACCTAAAAG TCTGATCATT  
65401 TTACATCTGT TCAGACATCT TTGAGCCCTT TCGGTGTCAG TTCCAAAGTT  
65451 GTTAGTGGGA ATTTCAAAGC CTTTAATAAT CTAGCCCCAC TTTGTTCACT  
65501 CTCTGTGTAA TAACCACATA CAACAATTGG CTGCATCTCC ATAGCACATG  
65551 GTACTCCTCC CGTTGCTTG GTTGTGCCAG CAACACTGGT TTTGCTTT  
65601 TCTTCCTGCT TGTGAGGTC ATTTCCAAGG CCCAGGTCTT TGTGCTTT  
65651 CCCAAGCTTC CCAGAGCTTC TTCCATACTC CCCTTACTTC CTGAGATT  
65701 ACTGTTCTCT CTTCAAGGCT TGTCTAGAA GAAGGAGGCA GCAGCAGCAC  
65751 TGTGGGTGAA TGGAAAGTGT ACCAGCTTG GAGTCAGACC ATTGGATCTC  
65801 AGCCCTACCA TTTTCTACTT AGATTTTTT AGGACAAATT TCTCCATCTT  
65851 TCTAAGCCTC CAATTGCTCA CTTACAAAAT TGATATAACA TTACCTTG  
65901 AAGATTGGTA TGGAAAGTAA TTAAACCACT ATTTAGAACAA TAGTAAATTAA  
65951 TAAATAACTA TTATTACCAT CATTACTATA GTTAGGACAC TCACTGTTAG  
66001 GTGCTATACA AAGAGGATCA TAAAAGGGAT GTTGTCTTGG GCTTCTTGG  
66051 ATAAATGTTG TCTTTTACT GTATTTAGA ATATCATTCT GGGTCATAAT  
66101 TGTGTTGTGT CATAATAATG AAACATACCTT GAATATTTAA TTACCTCTT  
66151 TTTTATTT TTAGCCATGT TAGAAGGTTG CCCACAGCTG AATATGGTTG  
66201 GCCTCTTCG ACGAATTATT TCCAAAGAAG GAATACCAAGG ACTTTACAGA  
66251 GGCATCACCC CAAACTTCAT GAAGGTGCTC CCTGCTGTAG GCATCAGTT  
66301 TGTGGTTTAT GAAAATATGA AGCAAACCTT AGGAGTAACC CAGAAATGAT  
66351 GTTGCACTTT TTGCTTCTAGC CTGATAATTG AAACCTTCAA CAATCTCTGG  
66401 AGTGAACCTT TCTCCTCGAA TTGAAACAAG TCTATGGCAA AAGAAGCTGC  
66451 ATTTTTTCA CAAAAGGGAA GATGGTAACA ATGGTCACCT CAAACTTTG  
66501 GGCTAAATTA TATGTACACA GAAATGTTCA AAATCATAGT TTTAATGTT  
66551 TTTGAAAGG CCACACAATT ATACTTTATC TTTTCTTAAT AATCCTGCAA  
66601 ATCTCTGCCA TGAATCCGAA ATCTGAAAT GTACTGGCTT GAACAAAATT  
66651 TGTGTTGTGT GTTAGAGTTA TAAATCATTAA ATCTTTATTT CGGGTGGTTT

66701 ACGTTTATGC CAGTCCTTT ATATTTAAAT TTCTTGTTT ATATATTTG  
66751 AATGTCCTTA TAGATTTCTT TAAATTCCT TATAGAACCA TTAATAGAAA  
66801 ATCATTACAT TTAAATATA CCTTACAGCA AAAGCATCCA AATAAGTATA  
66851 GGGTTTATGT CCTTATTTT CTTTCAGCTG AATACGAATG AGCACAGTGG  
66901 TGGAAATTCT GAAGGGAACT GATGAAATTAT TATTTATTC AGTGGGCACT  
66951 TTTCATTTT ACCACTGTAC CATTATTTGG TTCTGGAGT TATACACTAA  
67001 TTTCAGTAT ATTACTGTT AATTACCAAC ACAAGGCAAT TTATTTGAAA  
67051 GATTCGTTT ATCCTGCCAT TGCTTGAAA AGCAGCAGGA AACGAAATCC  
67101 TTGACTTGT ATCAGCTTCT GCAGAGCATC TTGTTTCC TTGTCCTTT  
67151 GTTCTTACCC TTGAAATCA GATTCGTTT TAGTCAGGAA GACTCTTGG  
67201 GACCACTCTT AGAACCTGA AATTCTTTT TAAATTGCT GAAAGTGGATT  
67251 GATCATGAGC AAATGATGT CTTATTCCTC CCTCACTGTT GAATATCTT  
67301 GAACTTGCTG TTTCAATAT GGGCAGCACA AAGGTGAGAG ATACATATTA  
67351 ATAGTAGTAT GTATTACTCT TATACATTAG ATACCTATAT TTAAATGAAA  
67401 GGCCAAATTG GTAAACATAT ACATTCAAT TCTCTCTTGC CCCAAGTTT  
67451 AGGAACATGT TAGGATATAG GAGACTTAAT TTATAATAAT GAGAGCATT  
67501 TTATTTTA CAAAGCCAT TTATAGTC AACTATCTT TCTTATTTGT  
67551 GTGATTAGAA CTTAGAAAAA TATTACTAG TTGAAGTTAT TATCAGTTT  
67601 TAATTTAGTT CTTAAACTCA TTCACTTCT AATAATTCT GTTATAAAATT  
67651 GCCAGCATT TAATGATGT AATAGGCATT TTCTTATTT  
67701 GAACCTACCT TTGAAACCAAA GAGAAAGATG GACTGGTGT  
67751 TGTGAAACAT TTTAAAAAT GTAGTTCAT TTATATTAGT TATGTTTGAT  
67801 AAATGTCCTCA GTATTTTAT AATATGATAA GCCTGGGATT CTACTTTAG  
67851 GGTATTTGT ACTTTGAGT AATATATAAA GTGACAATAT TAAGGTACAT  
67901 GATCAGCTCT TTCTATTTT ACTCGAAAA ATTATGGAAA TGAATAATT  
67951 TGCTAACAC TTTGAAATT CAAACCTCTG GAAAATATGA AAATATTCT  
68001 TGTTCAATT GAATTAAAT TGTAAGGTAT GAATGTGATT TGTCTGTACA  
68051 TCTTGATCT TTCCAAAAAA ATGATTCTG ATCTTTGGA AAAAAGCCGA  
68101 GAGTTGAAGA TAGTATATT CTGGTAGTAC TGAATATTAA CTTACAGTTT  
68151 CTATCAAAAAA TATATATTG TTTCTAAAAT TACTTGTTTT CCAGTTTTA  
68201 TTTTTTTAG AGAAAATTCT TAAGTCTCAG TTCTTAATT GAAAAAAA  
68251 AATTATAAAAT AAAGCAAAAAA TTGTATCTA CAGCTTAGCT AGCTTAGATG  
68301 TTGGCACCA GTTGAATCA TGCTTTTAC AGCTGGCTCC ATGTAAGTCTT  
68351 TCCAAACATT TTGGCCTTTC CTGAGCAGCC CTTGTAGATA TTGTCGTAT  
68401 GATGCATTTT GACACAAGGT GATATTTTT GTGATATCAA AATTCCACAT  
68451 TTACCCATTAA GAGTTACAGC CCTGGGGTTC ACAGTACCAA GGGGGACCCA  
68501 GAGCCTCAGG ATTGGCCAGG CTCACTTGC CGTGGAGTAT CAGTTGTCT  
68551 TGAAATTGTG GGAAAAAATT CTAAGTTGAA TTCACTGGTA AGTAATT  
68601 TAAAATTCA TAATGAGAT TACATCCAA ATTGATTAA AAAATTAAAA  
68651 CATAAGACTG CAGAGAAATT CTGCATTTCA ACTCCAATAC TATCCAGACT  
68701 TCAGAAATAA CTTATCAGTT ATTCTGTAA GCTTCTTGCT TACCTGGATA  
68751 CCTGACAGGT GAGATGGCTG TAGCAGACAC TGGCAGTTCC CTGCCACAC  
68801 ACCTGTCCT GTCCACAGCT GCACAAGGCA GCTCTGTGTG CAATTGCCAG  
68851 CATCTGCTCC TCTGTTCTA GGGAAATCTT GTAGAAAAAA TGCTGCCATA  
68901 TTGTTTCTC ACCTATTAGT CTTGTCCTCC AGTCAAGAGA ATAAATT  
68951 GCAAGCAGAG ATTGACTTT ACAGTATTGT GTCTTGAGC TTGGCATTAG  
69001 GTTCGATTG TAAAAATGTG GCATGGCTTC CTCACTCCCC AATAGGAAC  
69051 TTGCCAGCCCC TTTGTTCTC ATGGAACCTC CTTTTTGAA AAGAGCACCA  
69101 AAGGAGTAAAT AACTCTGTGG AGGGAGCAAC CCTCCCTTGC CATATGCTCT  
69151 CATTGGGAGA CATGTGGAGC AGTCTGAAGT CATTAGGCC ACTCTCTGGG  
69201 AGAGCACATC CTATGATGTT CTCCAGCCT AGCCCTTCC ACTGTGCTCA  
69251 AGTCCAAGCT GACCAGCTT CTGACCACAG TGAAACAAA GATGATTGTC  
69301 AGTGGCCCC AGAATCCTAT ACCCAGA (SEQ ID NO:3)

FEATURES:

Start: 2132  
Exon: 2132-2314  
Intron: 2315-17055

FIGURE 3X

Exon: 17056-17182  
Intron: 17183-20983  
Exon: 20984-21071  
Intron: 21072-41719  
Exon: 41720-41831  
Intron: 41832-45391  
Exon: 45392-45550  
Intron: 45551-47878  
Exon: 47879-48031  
Intron: 48032-54612  
Exon: 54613-54720  
Intron: 54721-59290  
Exon: 59291-59458  
Intron: 59459-63791  
Exon: 63792-63942  
Intron: 63943-66164  
Exon: 66165-66346  
Stop: 66347.

CHROMOSOME MAP POSITION:  
Chromosome 1

ALLELIC VARIANTS (SNPs):

DNA

Position	Major	Minor	Domain
1722	G	C A	Beyond ORF(5')
1767	C	G A	Beyond ORF(5')
1840	C	G	Beyond ORF(5')
1857	T	G	Beyond ORF(5')
1945	G	T	Beyond ORF(5')
2007	A	C	Beyond ORF(5')
2769	C	G	Intron
3664	C	T	Intron
3827	G	A	Intron
4113	C	T	Intron
4337	A	G	Intron
4473	G	A	Intron
6455	T	G	Intron
6533	T	G A	Intron
6919	G	C	Intron
7305	G	A	Intron
7340	A	G	Intron
7466	A	G	Intron
7589	G	C	Intron
7810	A	C	Intron
9104	G	A	Intron
9503	A	T	Intron
9898	G	C	Intron
10196	T	C	Intron
12327	C	G A	Intron
13749	G	A	Intron
14150	T	C	Intron
14529	G	A	Intron
14653	G	A	Intron
15871	A	G	Intron
19244	G	A	Intron
19387	T	G	Intron

FIGURE 3Y

19447	C	G	Intron
20076	T	C	Intron
20492	T	-	Intron
20868	T	C	Intron
20941	T	C	Intron
21116	C	T	Intron
21701	G	A	Intron
21710	A	-	Intron
21826	C	T	Intron
21840	-	T	Intron
21841	-	C T	Intron
21843	-	C	Intron
22045	C	A T	Intron
22061	G	T	Intron
22348	-	A G	Intron
22682	A	G T	Intron
22783	-	T	Intron
23448	A	G	Intron
24960	G	A	Intron
24983	T	C	Intron
25390	T	C	Intron
26060	C	T	Intron
30245	C	G	Intron
33664	G	T	Intron
33883	C	A	Intron
34373	G	A	Intron
34558	G	T	Intron
43929	T	A	Intron
44309	T	- C	Intron
44997	T	G	Intron
46538	A	G	Intron
48153	T	C	Intron
48288	G	T	Intron
48412	G	A	Intron
48446	C	G	Intron
48456	G	C	Intron
48789	C	-	Intron
48859	G	C	Intron
49126	A	G	Intron
49378	T	G	Intron
49482	A	C	Intron
49741	G	A	Intron
49840	A	G	Intron
50102	G	A	Intron
50109	C	G T	Intron
50747	G	A	Intron
51272	G	A	Intron
52842	G	A	Intron
61837	A	G	Intron
62018	A	G	Intron
65562	A	G	Intron
65780	G	A	Intron
66092	G	A	Intron
66617	C	T	Beyond ORF(3')
66892	G	A	Beyond ORF(3')
67263	G	A	Beyond ORF(3')
67651	G	T	Beyond ORF(3')
67935	C	T	Beyond ORF(3')

FIGURE 3Z

69000 T G Beyond ORF(3')  
69134 C T Beyond ORF(3')

Context:

DNA  
Position  
1722

TTGCCACGAGATGGCTTTGATCTTCTGCAACAAATCCAGGAGTTCTCCCTTGT  
TTTATAATTGCTCCAATAGATGTTAGGATTTAACCTCTGCTTTAAAGCAGAAC  
GCCATCCCAGGTGTGCAACCAACGAAAAAATTAGACATCCGTGAGAGACAATGCCCTCCAT  
GGCCCAGTTCCAGGAGAGAGAACGAGCTCTGGGCTGACCGCCAAGGCTCCGGCCGAG  
AGGGTCTTAAGTGGAGTAACCAGTCTCAAGACCCCGCTCCAAGCCACCGACGCGCTG  
[G, C, A].

(SEQ ID NO:35)

1767

AGTTTCTCTTTTGTTTATAATTGCTCCAATAGATGTTAGGATTTAACCTCTGCT  
TTTAAAGCAGAACATGCCATCCCAGGTGTGCAACCAACGAAAAAATTAGACATCCGTGAGA  
GACAATGCCCTCCATGGCCCAGTTCCAGGAGAGAGAACGAGCTCTGGGCTGACCGCCA  
AGGCTCCGGCCCGAGAGGGTCTTAAGTGGAGTAACCAGTCTCAAGACCCCGCTCCAA  
GCCACCGACGCGCTGACGCTGAGCCCTGACCTGCTGGGGCCTCTCCTCGGACCCGC  
[C, G, A].

(SEQ ID NO:36)

1840

TCGCCATCCCAGGTGTGCAACCAACGAAAAAATTAGACATCCGTGAGAGACAATGCCCTCC  
ATGGCCCAGTTCCAGGAGAGAGAACGAGCTCTGGGCTGACCGCCAAGGCTCCGGCCCG  
AGAGGGTCTTAAGTGGAGTAACCAGTCTCAAGACCCCGCTCCAAGCCACCGACGCG  
TGACGCTGAGCCCTGGACCTGCTGGGGCCTCTCCTCGGACCCGATGCTGACAGCG  
GAUTGGCAACTGGCAGAGGTGACCCGGTCCGACAGCACCTCCGAGACCCAGCTC  
[C, G].

(SEQ ID NO:37)

1857

CAACCACGAAAAAATTAGACATCCGTGAGAGACAATGCCCTCCATGGCCCAGTTCCAGG  
CAGAGAGAACGAGCTCTGGGCTGACCGCCAAGGCTCCGGCCGAGAGGGTCTTAAGTGG  
AGTAACCACTCTCAAGACCCCGCTCCAAGCCACCGACGCGCTGACGCTGAGCCCTGG  
ACCTGCTGGGGCCTCTCCTCGGACCCGATGCTGACAGCGGACTGGCAACTGGCAG  
AGGTGACCCCGGGTCCGACAGCACCTCCGAGACCCAGCTCCAGCTCCCTCACTTCC  
[T, G].

(SEQ ID NO:38)

1945

CAAGGCTCCGGCCCGAGAGGGTCTTAAGTGGAGTAACCAGTCTCAAGACCCCGCTCCC  
AAGCCACCGACGCGCTGACGCTGAGCCCTGGACCTGCTGGGGCCTCTCCTCGGACCC

GCATGCTGACAGCGGGACTGGCAACTGGGAGAGGTGACCCCCGGTCCGACAGCACCT  
CCGAGACCCAGCTCCAGCTCCCTCACTCCGGCTCTGGAGGGCCGGCCAGTG  
CCGCGAGGCCAGCGCGAGCTCCCTCCAGCAGCGGGACGCCACACCCCTGC  
[G, T].  
CCGCGCGGGCTCGGGTGGGTCTCGCTCTGCACCCCTGCACGGCAGCCGACCCCG  
ACGGCGCCCCAAACGCTGTTGCACGGCCGGCCAGCCGCTCGCCTGGTCCC  
GGTCTCGCCCCGAGCCCTCGATCTCCCGTACTTCCTCGCCAGGCCCTGCCCT  
GGGACCATGTTGCCTGGCTGCCAGGACTTCCTGCTGCCACCGCCGCTGCCAGGACGCC  
GAGCAGCCGACGCCAGCAGGCCCTTCAGGACTGGACCGCAATGGGACGGAGTG  
(SEQ ID NO:39)

2007 . . . . . GCCACCGACGCCAGCTGACGCTGCAGCCCTGGACCTGCTGGGGCCTCTCCCGAACCGC  
ATGCTGACAGCGGGACTGGCAACTGGGAGAGGTGACCCCCGGTCCGACAGCACCTCC  
CGAGACCCAGCTCCAGCTCCCTCACTCCGGCTCTGGAGGGCCGGCCAGTGCC  
GCCGAGGCCAGCGCGAGCTCCCTCCAGCAGCGGGAGGCCACACCCCTGCCGC  
CGCGCGGGCTCGGGTGGGTCTCGCTCCCGCCCTGCCAGCCGACCCGA  
[A, C].  
GGCGCCCCAAACGCTGTTGCACGGCCGCGCCCGCCAGCCGGCCTCGCCTGGTCCC  
TCTCGCCCCGAGCCCTCGATCTCCCGTACTTCCTCGCCAGGCCCTGCCCT  
GACCATGTTGCCTGGCTGCCAGGACTTCCTGCTGCCACCGCCGCTGCCAGGACGCC  
GCAGCCGACGCCAGCAGGCCCTTCAGGACTGGACCGCAATGGGACGGAGTG  
GGACATCGCGAGCTGCAGGAGGGCTAGGAACCTGGCATCCCTCTGGCCAGGACGC  
(SEQ ID NO:40)

2769 . . . . . TGGGGCCCGGACCGGCACCCCGTAACAGAAGTGGGTATAATACGAAAGTCTACTGGT  
ATTTGTCAGATAAAATGAGTGTGGACACTCTGGCCACGGGACTGTTAAATT  
AAGACACTTTGTCCTGAATCCATCCCAGGTTCTTGTGTTAATACCTTGAG  
ACATGTAATCCGTTTAGCTGTCAGACTTCAGTGGTCCCAAGTTGTATAAAGGCC  
CACATTGATCTTCAAGCTGCTTGTACAGCAGCTATGTTATTGCTACTGTT  
[C, G].  
AAAACGTTGAAACCAATCGCTGTTCCCCACTTCCTGTTGAGAAGGAATGGCGC  
ATTCATTGTTAAGACATTCTAGGTTAATGCCCTAGGTACATAAATTGATCTGAAGGG  
TTGACTTGACCTGCGACTGAGCAATTCTCTGAGTCATCTTAACCTGCCCC  
AACTTCTGCCCTTAGTAGGGGGAGATATGGAACCTCTCAACCCCTGTAAGCGT  
TCCCTGACACTGGCATTCTTATCCAAAGAGGGAAAGTGATTAGGTTACTATGAGGGCC  
(SEQ ID NO:41)

3664 . . . . . GCTGATTGCTCCAGAAATGGCCAGTTGGAGTCCCCACCATGCTCAATCATTGGCTGG  
AGCAGCCCAAGGAAAGGGACGACCTGCTGCAGTGATCAGCAGATGCCAGGGTTAGAGGC  
TAGAGAGTGGAAAGTCACCTGTTCCCTCACAGTAGGTGCTTGAAGGGAGATCTCAGTG  
GTACAACCTCCATGGTCCCTACAATATAACAAAGCTTTGGAGTGCTCAATGATTAA  
GATTGTAAGGGATCTGAGATCAAAAGCTTGAGAATTGCTGCTGTATCACCATT  
[C, T].  
GTAACGCTCATATTCTTTATATGTTGTCTAGTATATGTTACCAATTCTTTA  
AATCACCTTTACTTTATTGATAGTTAAAAGATTGTAAGTGAATTGCAATGGATGT  
CCTTGTATTCTATTCTCATTCTGGTCCAGTTACTTCCTGAGGATAATTGAGGAGT  
GGACATTGCTGAGCTGAGGTAACACACATTAAACTGGGATACGTTGCTTTCGG  
AAACCTTAGACCCATTCTCACTCTTGTACTGACAGTGCTTCTCCACATCCTCGCT  
(SEQ ID NO:42)

3827 . . . . . GAAGGGAGATCTCAGTGGTACAACCTCCATGGCTCTACAATATAACAAAGCTTTGGAG  
TGCTCAATGATTAAAGATTGAAAGGGATCCTGAGATCAAAAGCTTGAGAATTGCTG  
CTGTATCACCATTCTACGTAACCTGCTCATATTCTGTTATATGTTGTCTAGTATA  
TGTTACCAATTCTTTAAATCACCTTTACTTTATTGATAGTTAAAACGATTGTAAG  
TGAAATTGCAATGGATGTCCTTGTATTCTTCTCATTCTGGTCCAGTTACTTCGTA  
[G, A].  
GATAAATTGAGGAGTGGACATTGCTGAGTCTGAAGGTAAACACACATTAAACTGGGA  
TACGTATTGCCCTCGAAACCTTAGACCCATTCTACTCTTGAATGACAGTGCTTGC  
TTCTCCACATCCTCGCTCATTCTGGTATCAGTCTTGTAAAGTCTCTTCTGAGG  
GAAATTCTTTCTTCTGCTTAGTCCATTAGTGTGCTATAGTGGAAATATCTGAG  
ACAGGGTAATTATAAAGAAAAGACATTATTAGCTCACAGTCCGCAGGCTGGGAAGT  
(SEQ ID NO:43)

4113

CAGTTACTTCGAGGATAAAATTTGAGGAGTGGACATTGCTGAGTCTGAAGGTAAACACA  
CATTTTAAACTGGGATACTGCTTTCGGAAACCTTAGACCCATTTCACTCCTTGC  
ACTGACAGTGTCTGCCTCCACATCCTCGCTCATTAGGGTATCAGTCTTGAAAGTC  
TCCTATTCTGCAGGTGAAATTCCTTCTAGTCTAGTCATTAGTGTGCTAT  
AGTGAATATCTGAGACAGGGTAATTATAAAGAAAAGACATTATTTAGCTCACAGTTC  
[C, T]  
GCAGGCTGGAGTTAAGAAGCGTGGTGCCTGGCATCTGCTGGACTCCTGGGGAGGGCTT  
TCCTGCTGTGTCACAAACATGGTGGAAAGTCAAAGTGGAGTGGACATGTGTGAAGAAGCA  
AAATCCGAGGGGTGCTGGCTTATAGCAACCCAGCCTGAGGGAACTGATCCATTACT  
GAGGGAACTAATTCACTCATGAGAGAGAGAACTCACTCACTGCAAGAATGACACC  
AAGCCATTATGAGGGATCTGCCTCCGTAAACCTGACACCTCCTGCTAGGTCCCTCCTCC

(SEQ ID NO:44)

4337

CATTTAGTGTGCTATAGTGGAAATATCTGAGACAGGGTAATTATAAAGAAAAGACATT  
ATTTAGCTCACAGTCCGCAGGCTGGGAAGTTAAGAAGCGTGGTGCCTGGCATCTGCTGG  
ACTCCTGGGGAGGGCTTCCTGCTGTGTCACAAACATGGTGGAAAGTCAAAGTGGAGTGG  
ACATGTGTGAAGAAGCAAATCCGAGGGGTGCTCTGGCTTATAGCAACCCAGCCTGAG  
GGAACGTATCCATTACTGAGGGAACTAATTCACTCATGAGAGAGAGAACTCACTCACT  
[A, G]  
CTGCAAGAATGACACCAAGCCATTATGAGGGATCTGCCTCCGTAAACCTGACACCTCCT  
GCTAGGTCCCTCCCTCCACACCGGCACATCAGGGATCAGACTTCAACATGAGTTTGT  
GGGGACAAACAAACAGTAGCATTGCTTGCCTTGGTTCTATTACATCCTCCACAGG  
ATTGCTATTGCCTACCCATTGGTGGCAGTCTCTTAAATTGGTTACTGATTCAA  
ATGCTACCCCTCCTCCAGAGACATCCTCACAGACACACCCAGAAATCATGTTTACAGTT

(SEQ ID NO:45)

4473

TTCCCTGCTGTGTCACAAACATGGTGGAAAGTCAAAGTGGAGTGGACATGTGTGAAGAAGC  
AAAATCCGAGGGGTGCTGGCTTATAGCAACCCAGCCTCGAGGGAACTGATCCATTAC  
TGAGGGAACTAATTCACTCATGAGAGAGAGAACTCACTCACTGCAAGAATGACAC  
CAAGCCATTATGAGGGATCTGCCTCCGTAAACCTGACACCTCCTGCTAGGTCCCTCCTC  
CCAACACGGGCACATCAGGGATCAGACTTCAACATGAGTTTGTGGGGACAAACAAAC  
[G, A]  
TAGCACTTGCTTTGCCTTGGTTCTATTACATCCTCACAGGATTGCTATTGCCTAC  
CCATTGGTGAGGGCAGTCTCTTAAATTGGTTACTGATTCAAATGCTACCCCTCCTCA  
GAGACATCCTCACAGACACACCCAGAAATCATGTTTACCAAGTTATCTGGGATCCCTTA  
GTCCAGACGAGTTGATAACATAAAATTAAACCATCACACATGGGATAGAATTAGGATTACAC  
AGTCAACCTTATGGGAGAAAATTTCAGAGGCATGTCAGGGTTATGTAATGTCAAGGA

(SEQ ID NO:46)

6455

TGTTTATTGCTTGTGAGTGGAAATCAGGATTTCACTCCATTAAAGTAATTCCCTGTAAACAA  
AGAGGGTTCATTTCTTTTATTCATTAATATTGCTTTTTTTTTCTGGAGAC  
AGAATCTGCTCTATCACCAAGGCTGGAGTGCAGTGGTGCATCTGGCTCACTGCAGCC  
TCTGCTTCTGGATTCAAGCATTCTGTGCTCAGCCTCCCAAGCAGCTGAGATTACAG  
GCACATGCCACCACACCTGGTTAACCTTGTATTCTAGTAGAGATGGGATTGGCAT  
[T, G]  
TTGGTCAGGCTGGTCTGAAATTCTGGCTCTAGTGTCTGCCTGCCTCTGGCTTGAAA  
GTGCTAAGATTACAGGCATGAGCTACCATGGCCAGCCATTCCCTAAATATTAAATTGT  
CAGACATGTTATGGTTCTGGCACAATATTAAAGAAGACATGATGAAATCACAGGGTGA  
ATTTTAGGGCATCACACAGAAAGATTATGGTATAAGAAAAACATGGAATTCCAAC  
ATTCTGTCAAATGTTCTAAAATATAAAATCTGTATCTTGTGTTCTCCTGATT

(SEQ ID NO:47)

6533

TTATTTCTTAAATATTGCTTTTCTGGAGACAGAATCTGCTCTATCAC  
CAAGGCTGGAGTGCAGTGGTGCATCTGGCTCACTGCAGCCTCTGCTTCTGGATTCAA  
GGCATTCTGTGCTCAGCCTCCCAAGCAGCTGAGATTACAGGCACATGCCACACCT  
GGTTAACCTTGTATTCTAGTAGAGATGGGATTGGCATGTTGGTCAGGCTGGCTT  
GAATTCCCTGGCTCTAGTGTCTGCCTGCTCTGAAAGTGTAAAGATTACAGGC  
[T, G, A]  
TGAGCTACCATGGCAGCCATTCCCTAAATATTAAATTGTCAAGACATGTTATGGTTTC  
TGGCACAATATTAAAGAAGACATGATGAAATCACAGGGTGAATTGGCATCACAAC  
AGAAAGATTATGGTATAAGAAAAACATGGAATTCCAACACATTCTGTAAATGTTCT  
AAAATATATAAAATCTGTATCTTGTGTTCTCCTGATTATCTAAATTTGATGT

TATCCTTCTCTGAGAAATAAAGTGTCTGAAAGAATGAAAAAAATGGAAGAATTCTTAG (SEQ ID NO:48)

6919

ATGAAATCACAGGGTAATTTAGGGCATCACACAGAAAGATTATGGTATAAGAAAAAC  
AATGGAATTCCAACATTTCTGTCAAATGTTCTAAATATAAAATCTGTATCTT  
GTGTCTCTCTGATTATATTCTAAATTGATGTTATCCTCTGAGAAATAAAGTG  
TCTGAAAGAATGAAAAAAATGGAAGAATTCTTAGTAAGGTATAAAATACCCCTCTATC  
TTTAGCATTCTAACGCTTTGTCACCTTCAAACATCCACATGCCATATTCCCTGA  
[G, C]  
TAGGCCACAGCCATGTACATTGATCCCTTATTTCTCTCTGCTGAGATTCTCTC  
ATTCCCCCTCTGCTGGTATATGATTGCCATTGTTAAGGGCCAACTCACCTTA  
TAATCTTCTAGCCACTTCTTATCGGTATTCCAGAAAAACAAAAGAAGCTCCACA  
AGACAACATTCTGTAATACACTGCTTAACCTCTTGAACCTGCTGAGTTAAAAATCTT  
ATCTTTTAAGGATTGAATGGAGTCCACCAAGGTATCTATATTGACAGGATTATGAAA

(SEQ ID NO:49)

7305

GATTGCCATTGTTAAGGCCCCAACTCACCTTATAATCTCTAGCCCACCTCTT  
TCGGTATTCAGAAAAACAAAAGAGCTCCACAAGACAACATTCTGTAATACACTGCT  
TAACCTCTTGTACCTGCTGAGTTCAAATCTTATCTTTTAAGGATTGAATGGAGTC  
CACCAAGGTATCTATATTGACAGGATTATGAAAACAAAAGGATTGTTGAGAAAGTT  
GAAGCCTAACCTGAAACGTGGATCATAGTGTACTACACATTAACGTGTTAGTGGAT  
[G, A]  
TAATAGTTATTATTAAGGCTGGAATCAGAACAGGGTCAAATGTTTCAACGCTTGC  
TAGACTGTGGCTTGGCATGTTATTAAATGCTGGAGGCTCAAATGTTAACTAGGAAT  
GGTAAGACCTACCCAGTAACCTAGCATAAATAGTAAATTCTTAAATGTTTCAA  
CAGTGCCAGACATTGTTAATGAACTGGGATATAGTGTGAACACACTGACAGCGTTC  
TTCATTGATTCTAAAACCCCTCCATAGTAAGTAGGTCTGTGTGTGAGGTGCA

(SEQ ID NO:50)

7340

TAATCTCTAGCCACTTCTTATCGTATTCCAGAAAAACAAAAGAGCTCCACA  
AGACAACATTCTGTAATACACTGCTTAACCTCTTGTACCTGCTGAGTTCAAATCTT  
ATCTTTTAAGGATTGAATGGAGTCCACCAAGGTATCTTATATTGACAGGATTATGAAA  
ACAAAAGGATTGTTGAGAAAGTTGAAGCCTAACTCTGAAACGTGGATCATAGTGT  
CTACACATTAACGTGTTAGTGGATGTAAGTTATTATTAAGGCTGTTGAATCAGAAC  
[A, G]  
GGGTTCAAATGTTTCAACGCTTGCTAGACTGTGGCTTGGCATGTTATTAAATGCTG  
GAGGCCTCAAATGTTAACTAGGAATGGTAAGACCTACCCAGTAACCTAGCATAAATAGTA  
AATTCTTAAATGTTTCAAACAGTGCCAGACATTGTTAATGAACTGGGATATA  
GTGGTGAACACACTGACAGCGTCTCATTGATTCTAAACCCCTCCATAGTAAGT  
AGGTCTGTGTGTGAGGTGATGGGAATAAAAATAATAAGCAAATAATGAAACAG

(SEQ ID NO:51)

7466

TTAAGGATTGAATGGAGTCCACCAAGGTATCTTATATTGACAGGATTATGAAAACAAA  
GGATTTGTTGAGAAAGTTGAAGCCTAACTCTGAAACGTGGATCATAGTGTACTACAC  
ATTAACGTGTTAGTGGATGTAATAGTTATTATTAAGGCTGTTGAATCAGAACAGGGTT  
CAAATGTTTCAACGCTTGCTAGACTGTGGCTTGGCATGTTATTAAATGCTGGAGGC  
CTCAAATGTTAACTAGGAATGGTAAGACCTACCCAGTAACCTAGCATAAATAGTAAATT  
[A, G]  
TTCATTAAATGTTTCAAACAGTGCCAGACATTGTTAATGAACTGGGATATAGTGGT  
AACACACACTGACAGCGTCTCATTGATTCTAAACCCCTCCATAGTAAGTAGGTCT  
GTGTGTGTGTAGGTGATGGGAATAAAAATAATAAGCAAATAATGAAACAGGGTAAT  
TTCAAAAAGCAGAAAGAGCTATTCAACAAAACCTGCTTTTATTAGATGAAACTCTC  
AACTCTATGGTTGTTCTCCTGTCAATTCTGTTAAATGCTGTCAGCCTGTTCCCTA

(SEQ ID NO:52)

7589

AACTGTTTAGTGGATGTAATAGTTATTATTAAGGCTGTTGAATCAGAACAGGGTCAA  
ATGTTTCAACGCTTGCTAGACTGTGGCTTGGCATGTTATTAAATGCTGGAGGCCTC  
AAATGTTAATAGGAATGGTAAGACCTACCCAGTAACCTAGCATAAATAGTAAATT  
CATTTAAATGTTTCAAACAGTGCCAGACATTGTTAATGAACTGGGATATAGTGGT  
CAACACTGACAGCGTCTCATTGATTCTAAACCCCTCCATAGTAAGTAGGTCTG  
[G, C]  
TGTGTGTGTAGGTGATGGGAATAAAAATAATAAGCAAATAATGAAACAGGGTAATT  
AAAAGCAGAAAGAGCTATTCAACAAAACCTGCTTTTATTAGATGAAACTCTAAC

TCTATGGTTGTTCTCTCTGTCAATTCTGTTAAATGCTGTCAAGCTGTTTCCTTATCA  
CCCTGGCCACGACTCTGTCTTTCTGTTGGCTCTGTAGACTCTAACCAAGGCTCATT  
CTCTGCCTGGTATCTGCCCTCTGTGGCTTTGCCACTACCTACATTTCTGTGTTGCA

(SEQ ID NO:53)

7810

CTGGGGATATAGTGGTGAACAAACACTGACAGCGTCTTCATTGTATTCTAAACCCCTCC  
CTATAGTAAGTAGGTCTGTGTGTGTAGGTGCATGGGAATAAAAAATAAGCA  
ATAATGAACAGGGTAATTCAAAAAGCAGAAAGAGCTATTCAACAAACTACCTGCCTT  
TATTAGATGAAACTCTCAACTCTATGGTTCTCTCTGTCAATTCTGTTAAATGCTG  
TCAGCCTGTTCCCTATCACCCCTGGCACGACTCTGTCTTTCTGTTGGCTCTGTAG  
[A, C]  
CTCTAACCCAAGGCTCATTCTGCCTGGCTATCTGCCCTCTGTGGCTCTTGCCACTAC  
CTACATTCTGTGTGCACAGGGAGGGACCTCCCTGTGGACATAAAATTCTCTTT  
TGAAAGAATTCTATTGATTGGGCCACAGCACATCTGTGAAACAGCATTAGACATTG  
CCACTGCTCAGCAGCTCTGGGGAAAATGTTACTGAGAAGCGTACAGTAGTTTTTG  
CTAACCATGGTCAACCTCCCTCCAGAGGGAAACCTATGAGTATTCAAGGACATGTGAT

(SEQ ID NO:54)

9104

TTAACAGAATTATTGAGAAACAGAAAAACAAATACTGTGTTCTCATTTACAGGGGAGC  
TAAACCTGGTAAATGGGGCATAAAAGATGGGAACAATAGACACTAGGGACTCCAAAAGG  
GGGGAGGGAGGGAGGGCAAGGGCTGAAAAGCTTCTACTGGGACTTTGTTACAAC  
CTGGGTGATGGCACGATTAGGAGCTAAACCCCAGTATCACACAGTATACCCCTGTAACA  
AGCTGATGGTGAACCCCTGAATCTACAATAAAATTATTTATTAAAAATCATTATA  
[G, A]  
GGATTTTAAAGAAGGATTCTAGACAGGTGCAGCCAAACAATTTTTAAATGTTG  
GCAGGCCGCCACGCCAGTCACCTATGTCGAATAGCCATGTCCAACATTCCCAACCT  
ACTTCTCTCCAAAAGAGAAGCTATACTTCAAGATGGCCCTGTGCTGGTTCTCCCTGGAA  
GTTTCTGGGGAAAGGGCTTGAGTTGGCCACTGGACTCTCCTGGAGTGGAGCCGG  
GCTTCTGATCAGACGTGAGTGAGGCACTCCGCGTCTCCAGCGCAGCCAGAGTG

(SEQ ID NO:55)

9503

CATGTCCCAACATTCCAACCTACTTCTCCAAAAGAGAAGCTATACTTCAGATGGCC  
CTGTGCTGGTTCTCCCTGGAGTTCTGGGAAAGGGCTTGAGTTGCCCCACTGGAC  
TCTTCCCTGGAGTGGAGGCCGGCTCTGATCAGACGTGAGTGAGGCACTCCGCG  
TCTCCAGCGCAGCCAGAGTCGGTCCACGCAGTCCGGTCTTGCGCCTCGCGCC  
TTTGCCTGAAGCCCTAGGATGAGCCCTCTCCCTCAGAGCTTAAACGATGAAGGTGC  
[A, T]  
TTGTGTTGGGCCCTGAGGGAGATGCTGTTAGGCCCTTCCACTGGACGTGTTG  
GTGGGAGAGATCCGTTCTGTCGGTCGCACTCCACCCCGCTGGGCTCACTCAGGCC  
GGAGCTGCGAGGGAGACATCCTCGATGGACTCCCTCACGGAGATCTTTGGTACCTG  
GACTATAACAAGGATGGACCTGGACATTGAGCTTCAGGAAGGCCCTGGAGGATGTA  
GGGCCATTCAATCTAGAGGAAGCGAAGGTGGGCTCACTGGGCTGTAATCAGAGAG

(SEQ ID NO:56)

9898

ACCCCGCTGGGCTCACTCAGGCCCGGGAGCTGGAGGGAGACATCCTCGATGGACTCC  
TCTACGGAGATCTCTTGGTACCTGGACTATAACAAGGATGGGACCTGGACATTGG  
AGCTTCAAGGAAGGCCCTGGAGGAATGAGGGCATTCAATCTCTAGAGGAAGCGAAGGTGG  
GTCTCACTGGGCTGTAATCAGAGAGACGTTGGGCTGGAGGCCCTGGAGGGCATTGGG  
CAGAGAGGGCAAAATTACATGTTGTCAGCTTGACCTGGCCCACTGCAGTGTTCAGGT  
[G, C]  
GTTGACCAAGCGTACCGTTATTAAGAATAACAACACAGCTAACACATTCTCAAGTATT  
TTTCTCCGTTTCTCTGGCTGTTAGGAAATCTCCAACCTCAGATTGCTCTCAAGATGT  
TGGCTACATACAGCCTTGTCTTAGGAGTCACCTTGTCAATGTGCTCACCTGTCATTAGT  
CACCCAGAGGGCGTCTAGGCTAAAGATGCGCCCTCCCCAGTTCAAGAGAACTGGAATAAT  
CACTCTACGTGATTGGAGTGGGTTGGTATTGGAAATTCTGATGTTATGTTTG

(SEQ ID NO:57)

10196

GTGGTTGACCAGCGTACCGTTATTAAGAATAACAACACAGCTAACACATTCTCAAGT  
ATTTTCTCCGTTTCTCTGGCTGTTAGGAAATCTCCAACCTCAGATTGCTCTCAAGA  
TGTGGCTACATACAGCCTTGTCTTAGGAGTCACCTTGTCAATGTGCTCACCTGTCATT  
AGTCACCCAGAGGGCGTCTAGGCTAAAGATGCGCCCTCCCCAGTTCAAGAGAACTGGAAT  
AATCACTCTACGTGATTGGAGTGGGTTGGTATTGGAAATTCTGATGTTATGTTTG  
[T, C]

GGTTTCTGTCCTGGAAGGGGGCACTGGAAGTGGCTTTACTCTGGGTTCACTAGTGC  
TGAGGTTCTCTATAATATGCCCTAATTGATAGACCTAGTATCAGTACCGAGCTTAGG  
CTAACCCCTCTCTCCCAAGGCTAACCTACAGGCTCTCTCAGCATGTTGCTTC  
GTACATACTCTATTGAGTATTCCAAGTCAATTTCATTTGAAATTATTATTGTATA  
TAATAATTACTTATAAGTATATTGCTTTGGATGTTGACCCGGTAGACTGGGAGAT

(SEQ ID NO:58)

12327

GTCATGTTATTAAATGCCCTGGAGGCCTCAAATGTTAAGGTAATGGTAAGACCTACCC  
AGTAACCTAGCATAAAATAGTAAATTCTTATGTTCAAACAGTGCCAGACATT  
GTTAATGAACGGGGATATAGTGGTGAACAACACTGACAGCGTTCTTCAATTGATTCTC  
AAAACCCCTCCCTATAGTAAAGTAGGTCTGTTGTTGAGGTGATGGGAATAAAAAA  
TAATAAGCAAAATAATGAACAATAAAATTATTAAATTTAAAAAAAGAAATGATACTTAC  
[C,G,A]  
TTGTCGTTAAAGATACAAAAGCAATAACTTTTATTGTGAAAATAGTCTGTTTGAAAC  
AATATATTGTTTGTGTTCTGAAAGTTGAGAAACTAAATATACGAAGAGATAATG  
GTCAGACCATAAATAAAATAGAACTTTGACTCAAATTTACAGCAGTCTGCCAGAAA  
CCAGCCCCTTATCTAAAATAACAGACCAAGGAAACCAAGCTGTTATGTCAGACTTATAGG  
AAGTCAGGTTGCTATCTCTAGAGACAATACACAAAGCTATGCAATACTGCTGTAACAGC

(SEQ ID NO:59)

13749

TACAGGGCGTAGGCCACCATGCCCATAGACTATATATTGATCTGATAACTGG  
TTCAGCTACTAAGTGACTAACAGCAAGTAGCATCTAGTGTGATATGCTGGACAAA  
GGACATTACCTCTGGCAGGATGGCACAGAATGTTGAGAGATTTATCATGCTACTCA  
GAATGGTGTGCAATTAAAATTATGAGTTGTTGTTCTGGAGTTTCCATTAAATAGT  
TCAGACCATGGATTGACCGCAGGTAACTGAAACTGTGGAGAGTGAAACTGTGGATAAGGG  
[G,A]  
GGACTATTGATTGTTAAAGTCAGACTCATTAGGCAATCATACTCTGATTGCCATCAG  
AAATGCTGCAGAAATATGGGTTAAAAAAACTGTTCAAAAATAGGTCAAGGGATGTCCTT  
TAACCTGTTACTTCCAAATGTTAGTGAACCTGTGGCCCCAAAGAGTGAAGGAACAAA  
TGACTAAGAGAAAATCTTGTTCAAGGATGACAGATTAAGGAAAGCAACTTGCTGAA  
CACTGAAAATCTTCCACTTGTAAAGATAACACAAACTGGCTAAACTGGTTGGAATGAA

(SEQ ID NO:60)

14150

ATAGGGTCAGGGATGTCCTTAACTTGTTACTTCCAAAATGTTAGTGAAAATGTGGCC  
CAAAGAGTGAAGGAAACAAATGACTAAGAGAAAATCTGTTTCAAGGATGACAGATTAA  
AAAGAAGCAACTTGTGAAACACTGAAATCTCTCCACTTGTAAAGATAACACAAAATGG  
CTAAAATGGTTGGAATGAATATGGCAACTCAAGTCTGCACAGAACTAACTTGTGATG  
TTACAGCCAAATTCCACCATATTAACTAACTCCCCCGGATTTACACATGA  
[T,C]  
CTGTGAGGTAGCATGAAGAGGTAACTATGCATGCCCTAAGGACTTGGAGACCTCCCTT  
TCCCTCCACCAATCACCCACTAATCCCAAGAATCCGCCCTAAACCTTCTAATAACTAC  
CTTAAAGCCAGCATAGGGAGACAGATTGAGCTGGACTCTGTCTTCTGTGGGTACCT  
TGCAATAAAAAGCTTTCTTCTCAACACCTGGTATTAGTATTGACTTCTAGTTCT  
CGGGCAGCAAGCCCCTTTGGTCGGTACTATTCTGTCGCTGATATTCCATTGGCCA  
[G,A]

(SEQ ID NO:61)

14529

ACTAATCCCAGAATCCGCCCCAAACCTTTCTAATAACTACCTAAAGCCAGCATAGGG  
AGACAGATTGAGCTGGACTCTGTCTTGTGGTCACCTGCCAATAAAAAGCTTTCT  
TTTCTCAACACCTGGTATTAGTATTGACTTCTAGTTCTAGTCACTGGCAGCAAGCCCC  
TGGTCGGTACTATTCTGTTGCTGATATTCCATTGGCAAATATAACCTCTTAGA  
TGAAAATCAGTACGTAATGGGCCACAGAATGCTGTGACATTCTCTGGATTATA  
[G,A]  
CAGGTTACTTACTGAATACCGTAGGCAGTTATAACACACTAAGTATTGTTGATCTAA  
CATAGAAAAGATAACGTTAAATGGTAATTCTCAACTTTAGTTGAGATTGGAG  
GGTATGTCACATTGTTACAAGGGTATATTGATGCTGAGCTGAGGTTGGGTACAATTG  
AACCCCTGTCACCCAGGTAGTGAACATAGTACCCAACTGATAATTCTCAACCCCTGCCA  
TTCCCTCCCCGTTCTGTAGTCCCCAGTTCTGCTTTCCCATTTATACCGTGTGCA

(SEQ ID NO:62)

14653

CTCAACACCTGGTATTAGTATTGACTTCTAGTTCTAGTCACTGGCAGCAAGCCCC  
CGGTGACTATTCTGTTGCTGATATTCCATTGGCAAATATAACCTCTAGTGA  
ACTTCAGTACGTAATGGGCCACAGAATGCTGTGACATTCTCTGGATTATAGCAG  
GTTACTTACTGAATACCGTAGGCAGTTATAACACACTAAGTATTGTTGATCTAAACAT

AGAAAAGATAACAGTAAAAATATGGAATTTTTCAACTTTAGTTGAGATTGGAGGGT  
[G,A]

TGTGCACATTTGTTACAAGGGTATATTGATGATGCTGAGGTTGGGTACAATTGAACC  
CTGTCACCCAGGTAGTGAGCATAGTACCCAATCGATAATTTTCAACCCCTGTCCATTCC  
CTCCCCGTTCTGTAGTCCCCAGTTCTGTTTCCATCTTATATCCGTGTGACCCCC  
ATGTTTGTCTCCATGTGTATGTGAGAACTTGTGGTTGGTTCTATTCTGCGTGTG  
ATTGCTTAGGATAATGGCCTTCAGCTGCATCCATGTTGCTGCAGAGGACGTGATTTTAT

(SEQ ID NO:63)

15871

AGGAGTTTATCAATTTATTAGCTTTCAAAGAACCATCTTTGGCTTGTAAATCCTC  
CCAATGGGTGTTTCTTTCTATTACTTTGCTCTTATTCCTTCAACTTCCTTTT  
GCTTAATTTAAAATAATTCTGAGATTGAGATAAGCCTCAATGATGGGTACCGATT  
CCAGTCTTCTCTTCTAATTATGCATTTAAACACAGAAATCTTCTCTAAGTGTAGC  
TTTAGTTGAGCTACAAGTTAGATCTGCTCTCAGTCTGGAGGTTGGAGATCTGACC  
[A,G].

TGACCATGAAACCATCCAGTCACAATGTGGCATTATTTTTAATTTTTTTTTTTT

TGAGATAGAGTTCACTCTATTGCTTAGGCTGGTGTGCAATGGTGGATCTGGCTCAC

AGCAACCTCCACCTCCCAGGTTCAAGCGATTCTTGCCTCAGCTCCCAAGTAGCTGGG

ATTACAGGCATGCCACCATGCCCAACTAATTGTATTTTATAGTAGAGATGGGGTTC

TCCATGTTGGTCAGGTTGGCTTGAACCTCCGACCTCAGGTGATCCGCCACCTCAGCCT

(SEQ ID NO:64)

19244

GTGGCATTATTGGTCATATTTTATTTAGACTCCCTAATGCAAAACATATACAGT  
TGATCCTCATTATTGGGGATTCTGTATTGCAAATTGCTACTCAATAAAATTTATCC  
CCAAAGTAACCCAAAATATATACTCACAGTACTTCCAGGCATTGACATGCACA  
GAGCAGTAAAAACTTGAGTTGCTCAGCATGTACATTCTAGTAGTAGAATAAGGCAAT

ACTCTGCTCTCTGTTCAAGTCTCTCATACTATTAACTAGCAAGTATCCCTCAAGGTCT

[G,A].

TTTGTGCCAGTTTGCATTTTGATTTGGTAATTCTTTAAATGTTCC  
CCAAAGGTAGTGTGAAGTGCTGCTAGTGTCTTAAGTGCAAGAAAGCCATAGCATGCC

TTATGGAGAAAATATATGCGTTGGATAAGCTTGCCTTAAATGTTAGTGAATCAA

CAGCACACATTAAATGAGGTGCCCTCAAACAGAAACAGACATAAGACATGGTTATGTATT

AATCAGTTGATGAAAGTGTGTAATCAGAGGCTCACAGGAACCTAACCCCTGTTTCTG

(SEQ ID NO:65)

19387

CTCACAGTACTTCCAGGCATTGACATGCACAGAGCAGTAAAAACTTGAGTTGC  
TCAGCATGTACATTCTAGCTAGTAGAATAAGGCAATACTCTGCCCTCTGTTCTGCTC  
TCATACTATTAACTAGCAAGTATCCCTTCAAGGTCTATTGTGCCAGTTTGCATT  
TTGTATTGTTGTAATTCTTTAAATGTTCCCAAAGGTAGTGCTGAAGTGCT  
GTCTAGTGTCTTAAGTGCAAGAAAGCCATAGCATGCCATTGGAGAAAATATGCGTT  
[T,G].

GATAAGCTTGCCTTAAATCAATGTTAGTGAATCAACAGCACACATTAAATGAGGTGCC

TTCAAACAGAAACAGACATAAGACATGGTTATGTATTAAATCAGTTGATGAAAGTGTGTA

ATCAGAGGCTCACAGGAACCTAACCCCTGTTTCTGCTAGGAACATGGTTGGTATTG

CTAATTCAAGTGTGCAATGAATATAGAACCTTATGGAAGATGATTGCTGTGAATAATGA

GAATTAACCATACTCTTAAAGAGTGCATTCTAAAGGAGAATATTCAAGAAGGGTATTG

(SEQ ID NO:66)

19447

TCAGCATGTACATTCTAGCTAGTAGAATAAGGCAATACTCTGCCCTCTGTTCTGCTC  
TCATACTATTAACTAGCAAGTATCCCTTCAAGGTCTATTGTGCCAGTTTGCATT  
TTGTATTGTTGTAATTCTTTAAATGTTCCCAAAGGTAGTGCTGAAGTGCT  
GTCTAGTGTCTTAAGTGCAAGAAAGCCATAGCATGCCATTGGAGAAAATATGCGTT  
GGATAAGCTTGCCTTAAATCAATGTTAGTGAATCAACAGCACACATTAAATGAGGTGC  
[C,G].

TTCAAACAGAAACAGACATAAGACATGGTTATGTATTAAATCAGTTGATGAAAGTGTGTA

ATCAGAGGCTCACAGGAACCTAACCCCTGTTTCTGCTAGGAACATGGTTGGTATTG

CTAATTCAAGTGTGCAATGAATATAGAACCTTATGGAAGATGATTGCTGTGAATAATGA

GAATTAACCATACTCTTAAAGAGTGCATTCTAAAGGAGAATATTCAAGAAGGGTATTG

CATAATTCTTAACTAACAGATGCTGCCCTCACTGCTTACATGGCCAGATTCTCAT

(SEQ ID NO:67)

20076

TCTCTAGAATCCTGTCATCTCTCCAGGGTCTTCTCAAGAAAGTCTATCCTTCAC  
CACTAACAGTAATTGGTCTCTCTTCTGGAGAAGTCAGTGTATGCTGCTTC

AGCACCGACCCCTCTTACTTTGTTTGTTCATTCTTTCATGTACAGTAGTCCTAG  
GATTCTCATGAGCCTGTGAGCTGCTAGAAGGAATACAGCAGTGCTTACATTATTGCTT  
CTATTTATTTCTATTTCTCTCCGTCTCTGATTGTTCTCCTCTGTCCACAAACA  
[T, C]  
GCTCTAACTTCCCTAGTATTAAGGAAATTTCTGCTTTGTTCTTTATCCCTGCTCC  
CTTATTTTACTGCCAGATTTTATTTATTTATTTGAGATGGAGTCTCACTC  
TGTCAACCAGGCTGGGGTGCAGTGGCGCAGTCAGCTCACTGCAACCTCCGCTCCAG  
CTTCAAGCAATTCTCTTCTTCTAGCCTCCAAAGTAGCTGGGATTATGGCACCTGCCACC  
ATGCTGGCTGATTTCTATTTAGTAGAGACGGGTTTACCATGTTGCCACACTG

(SEQ ID NO:68)

20492 CACTCTGTCACCCAGGCTGGGGTGCAGTGGCGCAGTCAGCTCACTGCAACCTCCGCT  
CCCAGCTTCAAGCAATTCTCTTCTAGCCTCCAAAGTAGCTGGGATTATGGCACCTG  
CCACCATGCCCTGGCTGATTTCTATTTAGTAGAGACGGGTTTACCATGTTGCCA  
CACTGCTCTCTAAGTGCACCTCAGGTGAACCACCCGCTCAGCTCCAAAGTGTGG  
GATTGCAGGTGTGAGTCAGTGTGCTGGCTTTACTGCCAGATTTAAAAGAATAGTC  
[T, -]  
GTGTTTAGCTCTATTTCTCATTTACTACTCTCTTAACTCAGTCATATATGATGTTT  
TGCATAGTAAATGCTAGTAATTATTTAAAGTAGAAATAGGTACTTTAAAATGAAT  
AGATCCTACTTTAAATTGAATTATCTGGAGTTAGAATATCTGATTGGATTAGTTC  
TGCTACTCTTAATTACATTACTGGTAAGGCCACTGTGAAGTCAGTCTCTGGAGGA  
ATATTATTTATCTATAAGGCTGTTACAATTACTGAATTAAAAGTGTATTTATTT  
(SEQ ID NO:69)

20868 TAGTAATTTATTAAGGAAATGAGAAATAGGTACTTTAAAATGAATAGATCCTACTTTAAT  
TGAATTTATCTGGAGTTAGAATATCTGATTGGATTAGTCTGCTACTCTTAATT  
ACATTACTTGGTAAGGCCACTTGTGAAGTCAGTCTCTGGAGGAATTATTTATCTAT  
AAGGCTGTTACAATTACTGAATTAAAATGTTATTTATTTAATGTTATTTGTTA  
CATTTTAGTATTGATGTTGGGATAGGCATTAAAGCAAGTCATAACTCACCTACATGCA  
[T, C]  
AATTTGCCCTAATCAGTTAAAGCTTCTTAAATGAGAGATTGAAATTCTATAATT  
CTGTGGCTTATCAGTCTGAGTTTATTTTGCCTTTTATTTTAAAGGAAA  
ATTGAGGCTTCAGAAATTGTCAGTCTCCAGACACTGGGCTGACTATTCTGAACAA  
CAAGCAGAGTTGATTCTCAAAGGTAAGCTTCTGTTGGTCAACAATTGACTTTCACT  
TTAATATCCTGCATTAGAACTCTGTTGTAAGTGTGGCTTTAAACACCTCCCTAGTC  
(SEQ ID NO:70)

20941 GAGTTAGAATATCTGATTGGATTAGTCTGCTACTCTTAATTACATTACTGGTA  
AGGCCACTTGTGAAGTCAGTCTCTGGAGGAATTATTTATCTATAAGGCTGTTACAA  
TTACTGAATTAAAATGTTATTTATTTAATGTTATTTGTTACATTAGTATT  
GATGTTGGGATAGGCATTAAAGCAAGTCATAACTCACCTACATGCTATAATTGCTTA  
ATCAGTTAAAGCTTCTTAAATGAGAGATTGAAATTCTATAATTCTGTTCTTA  
[T, C]  
CAGTTCTGAGTTTATTTTGCCTTTTATTTTAAAGGAAAATTGAGGCTTCAG  
AAATTGTCAGTCTCCAGACACTGGGCTGACTATTCTGAACAACAAGCAGAGTTGA  
TTCTTCAAAGGTAAGCTTCTGTTGGTCAACAATTGACTTTCACTTTAATATCCTGCA  
TTAGAACTCTGTTGTAAGTGTGGCTTTAAACACCTCCCTAGTCTCATTATGTTA  
TCCAAGATCTTTGCTTTCTCCCTCCATTCAATTGTTATGTCACATTATCTAAAG  
(SEQ ID NO:71)

21116 GTATTGATGTTGGGATAGGCATTAAAGCAAGTCATAACTCACCTACATGCTATAATT  
CTTAAATCAGTTAAAGCTTCTCTTAAATGAGAGATTGAAATTCTATAATTCTGTT  
TCTTATCAGTTCTGAGTTTATTTTGCCTTTTATTTTAAAGGAAAATTGAGG  
CTTCAGAAATTGTCAGTCTCCAGACACTGGGCTGACTATTCTGAACAACAAGCAG  
AGTTGATTCTCAAAGGTAAGCTTCTGTTGGTCAACAATTGACTTTCACTTTAATAT  
[C, T]  
CTGCATTAGAACTCTGTTGTAAGTGTGGCTTTAAACACCTCCCTAGTCTCATTAT  
GTATATCCAAGATCTTTGCTTTCTCCCTCCATTCAATTGTTATGTCACATTATC  
TAAAGTGTAAAGAATGGGAAGTGTAAAGCTCAGACTGGACTCTTCTTCAAGGCCCAAAG  
GATAGTGGAAATGGCAGGAAGTAAGGTTTAACTCATAGATGAGGAGCTGAAGAGTTG  
GTGTTGCTTTCTCCATTGTTCTAATGTCAGTAAACTCATTGATTCAAACCTAA  
(SEQ ID NO:72)

21701 CATTGATTCAAACAAAGAAGACTAGCAGATTCAACATTATTTAACCTAGATGTGACTG  
GAAAAAAAGGGAAATTACTAAGCTCTCAAGCTAACAAAGAAATACCTGTTAACCTTCA  
GAAAACAGAAATGCAAATTGAACTTATTGTCGGGCAATCAGTTGACTATTTAAGT  
CAGACTTTATACTCTTAATGTTGTTCATGGATAGAGCAGTAATCTCTGAGGCCA  
GGTGCTCTCAAATACTCTGTTGCTATAAACACAGGGCAGGAACGTGATTTTATGATAAC  
[G, A]  
TAAAACAGAAAAGGACAATTATTTGTTATTGTTGAAATATTCAGTCCTCAC  
ATTGTCATAAAATCTTCTAAATGGCTTGTATTGAAATTATCTCATTATATCTGTG  
CCAACAGCATTCTCCTTCTTCTATAATTCTTACAAACAGCTGCTCAAGAGGA  
AGGCTCAAAGTCTCAAGGCTGAGCACGTAATGACTTTGTTAGTACTAGATGAGAAGGGC  
TTTCTGAGGAATGAAAACCTAAAACATGAAAAGAAGATAAACAGAATTGGACAGTGA

(SEQ ID NO:73)

21710 AAACATAAGAAGACTAGCAGATTCAACATTATTTAACCTAGATGTGACTGGAAAAAGG  
GAAATTACTAAGCTCTCAAGCTAACAAAGAAATACCTGTTAACACTTCAAGAAAACAGA  
AATGCAAATTGAACTTATTGTCGGGCAATCAGTTGACTATTTAAGTCAGACTTT  
ATACTCTTAATGTTGTTCATGGATAGAGCAGTAATCTCTGAGGCCAGGTGCTCTC  
AAATACTCTGTTGCTATAAACACAGGGCAGGAACGTGATTTTATGATAACGTAACACAG  
[A, -]  
AAAGGACAATTATTTGTTATTGAAATATTGTTGAAATATTTCAGTCCTCACATTGCTAA  
AAATCTTCTAAATGGCTTGTATTGAAATTATCTCATTATATCTGTGCCAACAGCA  
TTTCTCCTTCTTCTATAATTCTTACAAACAGCTGCTCAAGAGGAAGGCTCAA  
GTCTCAAGGCTGAGCACGTAATGACTTTGTTAGTACTAGATGAGAAGGGCTTCTGAG  
GAAATGAAAACCTAAAACATGAAAAGAAGATAAACAGAATTGGACAGTGAAGATATAGAG

(SEQ ID NO:74)

21826 CAGAAATGCAAATTGAACTTATTGTCGGGCAATCAGTTGACTATTTAAGTCAGAC  
TTTATACTCTTAATGTTGTTCATGGATAGAGCAGTAATCTCTGAGGCCAGGTG  
TCTCAAATACTCTGTTGCTATAAACACAGGGCAGGAACGTGATTTTATGATAACGTAAC  
ACAGAAAAGGACAATTATTTGTTATTGAAATATTGTTGAAATATTTCAGTCCTCACATTG  
TCTAAAATCTTCTAAATGGCTTGTATTGAAATTATCTCATTATATCTGTGCCAA  
[C, T]  
AGCATTTCATCCTTCTTCTATAATTCTTACAAACAGCTGCTCAAGAGGAAGGCT  
CAAAGTCTCAAGGCTGAGCACGTAATGACTTTGTTAGTACTAGATGAGAAGGGCTTCC  
TGAGGAATGAAAACCTAAAACATGAAAAGAAGATAAACAGAATTGGACAGTGA  
AGGCATATAATATTCTGTTCTAAAGTAATATTCTCTAGGAAAGTGAGGGCTTCC  
TGGCTTGTAGGCCAGAAATCATATTCTATATTCTTGTAGCTTGTAGGAAATAATGCA

(SEQ ID NO:75)

21840 TGAACCTTATTGTCGGGCAATCAGTTGACTATTTAAGTCAGACTTTATACTCTTAA  
TGTTTGTTCATGGATAGAGCAGTAATCTCTGAGGCCAGGTGCTCTCAAATACTCTG  
TTGCTATAAACACAGGGCAGGAACGTGATTTTATGATAACGTAACAGAAAAGGACAA  
TTATATTGTTATTGAAATATTGTTGAAATATTTCAGTCCTCACATTGCTAAAAATCTTC  
TAAATGGCTTGTATTGAAATTATCTCATTATATCTGTGCCAACAGCATTCTCATCC  
[-, T]  
TTCTCTTCTATAATTCTTACAAACAGCTGCTCAAGAGGAAGGCTAAAGTCTCAAGGC  
TGAGCACGTAATGACTTTGTTAGTACTAGATGAGAAGGGCTTCTGAGGAATGAAA  
CCTAAACATGAAAAGAAGATAAACAGAATTGGACAGTGA  
TCTGTTCTAAAGTAATATTCTCTAGGAAAGTGAGGGCTTCCCTGGCTTGTAGGCCA  
GAAATCATATTCTATATTCTTGTAGCTTGTAGGAAATAATGCAAATTCTAAGGCCAA

(SEQ ID NO:76)

21841 GAACCTTATTGTCGGGCAATCAGTTGACTATTTAAGTCAGACTTTATACTCTTAA  
GTTTGTTCATGGATAGAGCAGTAATCTCTGAGGCCAGGTGCTCTCAAATACTCTG  
TGCTATAAACACAGGGCAGGAACGTGATTTTATGATAACGTAACAGAAAAGGACAA  
TATATTGTTATTGAAATATTGTTGAAATATTTCAGTCCTCACATTGCTAAAAATCTTC  
AAATGGCTTGTATTGAAATTATCTCATTATATCTGTGCCAACAGCATTCTCATCC  
[-, C, T]  
TCTCTTCTATAATTCTTACAAACAGCTGCTCAAGAGGAAGGCTAAAGTCTCAAGGC  
GAGCACGTAATGACTTTGTTAGTACTAGATGAGAAGGGCTTCTGAGGAATGAAAAC  
CTAAACATGAAAAGAAGATAAACAGAATTGGACAGTGA  
TCTGTTCTAAAGTAATATTCTCTAGGAAAGTGAGGGCTTCCCTGGCTTGTAGGCCAG

AAATCATATTCTATATTTCTTGTAGCTTAGGAATAATGCAAATTCTAAGCCAAG (SEQ ID NO:77)

21843 ACCTTATTGTCTGGGCAATCAGTTGACTATTTAAGTCAGACTTTATACTCTTAATGT  
TTTGTCTCATGGGATAGAGCAGTAATCTCTGCAGCCCAGGTGCTCTCAAATACTCTGTG  
CTATAAACACAGGGAGGAACGTGATTTTATGATAACGAAAACAGAAAAGGACAATTA  
TATTGTATTAATATTGTGTGAATATTTCTAGCCTCACATTGTCTAAAATCTTCTAA  
ATGGCTTGTATTGAATTATCTCATTTATATCTGTGCCAACAGCATTTCATCCTT  
[-, C].  
TCTTCATAATTTCTTACAAACAGCTGCTCAAGAGGAAGGCTCAAAGTCTCAAGGCTGA  
GCACGTAATGACTTTGTAGTACTAGATGAGAAGGGCTTCCCTGAGGAATGAAAACCT  
AAAACATGAAAAGAAGATAAACAGAATTGGACAGTGAGATATAGAGCATATAATATTCT  
GCTTCTAAAGTAATATTCTTAGGAAAGTGAGGGCTTCCCTGGCTTGTAGGCCAGAA  
ATCATATTCTATATTTCTTGTAGCTTAGGAATAATGCAAATTCTAAGCCAAGCT

(SEQ ID NO:78)

22045 ATATTTTCAGCTCACATTGTCTAAAAATCTTCTAAATGGCTTGTATTGAATTAT  
CTCATTTTATATCTGTGCCAACAGCATTTCATCTCTTCTCATATAATTCTTACAA  
ACAGCTGCTCAAGAGGAAGGCTCAAAGTCTCAAGGCTGAGCACGTAATGACTTTGTAG  
TACTAGATGAGAAGGGCTTCCCTGAGGAATGAAAACCTAAAACATGAAAAGAAGATAAA  
CAGAATTGGACAGTGAGATATAGAGCATATAATATTCTGCTCTAAAGTAATATTCTC  
[C, A, T].  
AGGAAAGTGAGGGCGTTCCCTGGCTTAGGCCAGAAATCATATTCTATATTTCTT  
GATAGCTTAGGAATAATGCAAATTCTAAGCCAAGCTCAGAATAGACTAAGAAGTATT  
AGCTTAGCTGCCATGACAAAATACCATAGGCTGGATGCATTAAACAATGAAAATTAGTT  
TTTCACAGGTCTGGAGCTGGGAAGTTAAGATGAGAGTGCCAGCATGGTTGGGTTGTAG  
TGAGGGCTCTTCTGGCTTGAGATAGACCCCTCTCACTGTATTGTATATGGCAGA  
(SEQ ID NO:79)

22061 CATTGTCTAAAATCTTCTAAATGGCTTGTATTGAATTATCTCATTTATATCTGT  
GCCAACAGCATTTCATCCTTCTTCTCATATAATTCTTACAAACAGCTGCTCAAGAGG  
AAGGCTCAAAGTCTCAAGGCTGAGCACGTAATGACTTTGTAGTACTAGATGAGAAGGG  
CTTCTGAGGAATGAAAACCTAAAACATGAAAAGAAGATAAACAGAATTGGACAGTG  
AGATATAGAGCATATAATATTCTGCTCTAAAGTAATATTCTCTAGGAAAGTGAGGGCG  
[G, T].  
TTCCCTGGCTGTAGGCCAGAAATCATATTCTATATTTCTTGTAGCTTAGGAATA  
ATGCAAATTCTAAGCCAAGCTCAGAATAGACTAAGAAGTATTAGCTTAGCTGCCATGA  
CAAATACCATAGGCTGGATGCATTAAACAATGAAAATTAGTTTACAGGTCTGGGA  
GCTGGGAAGTTAAGATGAGAGTGCCAGCATGGTTGGTTGTAGTGAGGGCTCTTCT  
GGCTTGAGATAGACCCCTCTCACTGTATTGTATATGGCAGAGAGAGAGAGAGAGA  
(SEQ ID NO:80)

22348 GAAAGTGAGGGCGTTCCCTGGCTGTAGGCCAGAAATCATATTCTATATTTCTTGT  
TAGCTTAGGAATAATGCAAATTCTAAGCCAAGCTCAGAATAGACTAAGAAGTATTAG  
CTTAGCTGCCATGACAAAATACCATAGGCTGGATGCATTAAACAATGAAAATTAGTTT  
TCACAGGTCTGGAGCTGGGAAGTTAAGATGAGAGTGCCAGCATGGTTGGGTTGTAGTG  
AGGGCTCTTCTGGCTTGAGATAGACCCCTCTCACTGTATTGTATATGGCAGAGA  
[-, A, G].  
AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGGGATCTTCTCTGCTTCTATTATAAGG  
CCATAGCTCTGTGGATCAGGGTCCATTCTTATGACTTTATTGACTTACCCCCCTAA  
GATGCTATCTCAGATATAATCACACGGTGGTTAGGGCCTAACATTTGGATTGGGAG  
GGACACAGCTCAGTCCATAGCAAAGGATAATGAGAGGGTTGGATATTAAAAGTAGCTA  
CACAATTAAATATAATATTGTAACTTTTTTTTTTGAGATGGAGTCTAG  
(SEQ ID NO:81)

22682 ATCTTCTCTGTCTTCTATTATAAGGCCATAGTCTGTGGATCAGGGTCCATTCTTA  
TGACTTATTGTACTTTACCCCCCTAAGATGCTATCTCAGATATAATCACACGGTGGGT  
TAGGGCCTAACATTGGATTGGAGGGACACAGCTCAGTCCATAGCAAAGGATAATGC  
AGAGGGTGGATATTAAAAGTAGCTACACAATTAAATATAATTTATGGTAACT  
TTTTTTTTTTGAGATGGAGTCTAGCTCTGCTGCCAGGCTGGAGCGCAATGGTGCAG  
[A, G, T].  
CTCAGCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAATTCTCTGCCCTAGCCTCTG  
AGTAGTTGGACTATAGGCACGCGCCACCAAGGCCCTGGCTATTTTTTTATTAACTA

GAGACGGGTTGCACCATATTGTCAGGCTGTCTGAACTCCTGACATCAGGTGATCCA  
CCCATCTGGCTCCAAAGTGCTGGGATTACAGAAGTGAGCCACCGCGCCTAGCCAGCA  
GCTTACTGAGATGTAATTACATGCCATAAATTCACTTTCTAAAGTATAACAATTCACT  
(SEQ ID NO:82)

22783 ATATAATCACACGGTGGTTAGGGCTCAACATTTGGATTTGGGAGGGACACAGCTCAGT  
CCATAGCAAAGGATAATGCAGAGGGTTGGATATTTAAAGTAGCTACACAATTAAATA  
TAAATATTTATGGTAACTTTTTTTTTGAGATGGAGTCTAGCTCTGTTGCCAGG  
CTGGAGCGCAATGGTGCATCTCAGCTCACTGCAACCTCCGCCCTCCACGGTCAAGCAAT  
TCTCCTGCCCTCAGCCTCTGAGTAGTTGGACTATAGGCACGCCACACGCCCTGGCTA  
[-, T]  
TTTTTTTTATTTTACTAGAGACGGGTTGCACCATATTGGTCAGGCTGTCTCGAACT  
CTTGACATCAGGTGATCCACCCATCTGGCTCCAAAGTGCTGGGATTACAGAAGTGAG  
CCACCGGCCCTAGCCAGCAGCTTACTGAGATGTAATTACATGCCATAAATTCACTTT  
CTAAAGTATAACAATTCACTGACTAAACATTATTTATTTAAATTGACAGAATTACA  
TGTATTTATCATGTACAACATGATGTTGAAGTATAATGTACATTGTGGAGTGACTAAGT  
(SEQ ID NO:83)

23448 TTCTCTTAGTATTTCAAGAAATAATAATTATTATTAAATTGAGTCTTCATGTTGA  
TAGTGGAGCTTGAACCTATTCTCATGTCAGCTGAAATTGTTGTCCTTTAACACAA  
ACCATACCCAGCTCCAAAGTATTCTGCTCTGCTTCTATGAGATTAACCTTTCTGAT  
TCCACATGAGTGAGATCATGCACTATTATTTGCTTACCTGGCTTATTCTTACATAT  
TGTACAGATAACAGGATTTCTCTTTTAATGGCGAATAGTTCTATTGTATAT  
[A, G]  
TATAGCACATTCTCTCATGCATTGGTGGACACTAGGTGATTCCGTATCTGGC  
TATCGTGAATAGTGTATAATGAAACATGGGAATGCACATGGCTTTGACATATTGATT  
CATTTATATATGTGTATATATATGTATACACACACATAACAGTGGTGGGATTGC  
AGGATCATATGGTAGTTCTATATTAAATTAAAGGAACCTCCATACTGCTTCCATAAT  
GGCTGTATTAGTTAACCTCTACCAACAGGGTCAAAAGTCCCTTTCTACATACT  
(SEQ ID NO:84)

24960 TTGTTCTAGAGTATAGTTAACTGATGTTCTTACTGATTTCTGTTGAGATGATT  
GTCTATTGCTGAAGGTAGGGTGTGAAGTCCCCTACTATTGCTGTATTGAGTCTCTC  
TCTTCTAGACGTATTAACTGGTTTATTATTTATTGTTGTTGTTGTTGTTGT  
TGTGTTTGAGACGGAGTCTCACTCTGTCACCGGGCTGGAGTGCAGTGGCAGGGTCTC  
GGCTCACTGCAGCCCGTCTACGGTTCAAGCGATTCTCCTGCCTAGCCTCCGAGTC  
[G, A]  
CTGGGACTACAGGGCATGCCACACGCCAGCTAATTGTTGTTAGTAAAGACGG  
GGTTTACCATGTTGCCAGGATGGCTTGATCTCTGACTTCTGATCCACCCGCTTG  
GCCTCCAAAGTGCTGGGATTACAGGTGAGCCACACCCCTGCCAATGTTGGTATT  
TATCTTAAAGTGCTGTATGTTGGGTCATATATATTATAAAACATAGCTACATAA  
CTTATTAAGGGATATGCAATATAAAATATAAAATTGACACTGAAATTAAATGGG  
(SEQ ID NO:85)

24983 TCTGATGTTCTTACTGATTTCTGTTGAGATGATTGCTATTGCTGAAGGGTAGGGTGT  
TGAAGTCCCCTACTATTGCTGTATTGAGTCTCTCTCTTCAAGACGTATTAAATGGTT  
TTTATTTTATTTATTGTTGTTGTTGTTGTTGTTGTTGAGACGGAGTCTC  
ACTCTGTCACCAAGGTGGAGTGCAGTGGCAGGGTCTGGCTCACTGCAACCCGCTCTA  
CGGTTCAAGCGATTCTCCTGCCTCAGCCTCCGAGTCGCTGGGACTACAGGGCATGCCA  
[T, C]  
CACGCCACGCTAATTGTTGTTAGTAAAGACGGGGTTTACCATGTTGCCAGGAT  
GGCTTGATCTGACTTCACTGATCCACCCGCTGGCCTCCAAAGTGCTGGGATTAC  
AGGTGTGAGCCACCAACCCCTGCCAATGTTGGTATTATCTTAAAGTGCTGTGTTG  
GGTTCAATATATATTATAAAACATAGCTACATAACTTAAAGGGATATGCAATATA  
AAATATATAAAATTGACACTGAAATTAAATGGGAGGAGTGGAGTAAAGTACCTTC  
(SEQ ID NO:86)

25390 AGTGTGGGATTACAGGTGTGAGCCACCAACCCCTGCCAATGTTGGTATTATCTTGT  
GTGCTGTGATGTTGGGTCATATATATTATAAAACATAGCTACATAACTTATAAG  
GGATATGCAATATAAAATATAAAATTGACACTGAAATTAAATGGGAGGAGTGG  
GTAAAAGTACCTTCATATAACTTACTATTATATCCTTATTGAATTGACCCCTTATCA  
TTATATAGGAACCTTGTGTTCTCCTTACAACCTCTGACTTAAAGTTGTTATATGATA  
[T, C].

AAGTAAAGTTACTCTGCTCTCTGGTTCTGTTCCATGGAATATCTTTTCCATTCTTCACCATCAGTCTGTGTATTTTACAGATGAAATGAGCTGTCTGGCAGCATATAAGTGGATCTAGTTTTTAATCCACTCAGACACTGTGTTTTGATTGGATAATTAACTCATTCTATGTTCAAGGTAAATTATTGATAAGTAAGGACTTGTACTACCATTGCTTATTGTTCATGGTTCTTTATAGATCCTTATTCTTTCTTCTCTCTGCTGTCCTTTTTT

(SEQ ID NO:87)

26060 GGTTTTGGTTTGTGGTACCAAGAGGTTACAAAAAACATCTTAAAGAGTTATAATAGTT  
ATTTAACCTGATAACTTAACTTATTGCAAAACCCCCAAAACAAAAAAATCTACAC  
TTTACTTAACTCCCTGAAATTGAAATTGATGTCACAGTTACCTCTTCATATT  
GTGTATCCCTAAATTATTGTAGCTATTACTTTAAATAGTTCTCTTCTACTAC  
AGATGTAAGTGTATTGCATACCATCATTACAGTATTATTGAAATTACCTGTGTACTTT  
[C, T]  
TTTATCAGCCAGTTTATCTTCAAGATGTTTGTGTTACTCATTAGCATCTTTCT  
TTCAGCTTGGAGAGCTCTTACGTTCTTATAAAATAGTGCCTCATGATTATCTC  
CTCAGCTATTGTTGTCGGAAAGTATCTCTCCTTCTTCTGAAGGACACTTGTGG  
GTACATTACCCCTGGTTGGTATTCTCTCCTTGAACGCTTAAATATATCATCCCTTCT  
CTCCTGACCTGTAGGTCTGCTGACCAGTCTGTTCCAACCATATTGGGACTGTCTTAA

(SEQ ID NO:88)

30245 ATTTAACCATCCATTGTTCTGCTCTAGATAACCCCTGACTAATATATAATTGGTAT  
GAAGTGATATCTCATGGCTTGATTTATATTCTTCTGGTAGTGACTTTTTGTAC  
TTTGGGATATTGTTATTATTATTATTACTAGTGTATACTCTCAGTAAA  
GTGTTAGAAACAATTAAAGGCAGAATGTGACCAAGGTTCCTGAGTTATATAACCA  
TCATGGACCTTCCCTCAAGTGCTAAGCCATTAGTGTACTCATGTCACTCCAAATGTCAG  
[C, G].  
TTGTTTCTCCATTCACTGCTCTTGTGTCCTAACTTGAATTCTATGGAAAAACAT  
CTGAATGGTGCTTAATATGGTTGGATATTGTCCTCCAAATCTCATGTTGAAATATG  
ACCTCCAGTGTGGAAAGTAGGGACTACTGGGTCAAGGAGAGTGGATCTTCATTAAATGGC  
TTGGTAATAAGTGAACTCTATTAGTTCATGAAAGCTGGTTGATAAGAGCCTGGATC  
TCATTCTCTGGCCTCTCACCATCTGACACACTTGTCACCTTTTCTCAGCCA

(SEQ ID NO:89)

33664 TTCCAGAGTGTAGAAGTACACTGCTTATCTTTCTAGGAGATCATTATAACACCAAAAG  
CAGACAGTATATGAAACAGGGAAATTAGAGGCCAGATACTTATGACTTATATGAAAAAA  
TTTAAAGAAAATATTAGCAAACTGAATCAGCCATTAAAAAAATACCCACATCAATGC  
ATTCTAAAGAGGAGCTTAAACAAAATTGTTAGAAGGCATTAAAGAAGACTCAGTATAGAA  
AAGATGTACCTCTCTCCAAATTGGTGATAGAGATTCAATGCCATTAAAAAAACCCACCT  
[G, T]  
GTTTTTTGAGGAACCTGTCAAGCTGAGTCTCAAATTATCAAAAGAGCAAAGGCCTAA  
GAATATCCAGGACATTCTGAAGAACGTAGGAGCCAGGGGCTGCCCTATCAGATACC  
AAGGGTTGTTATAAGCCATAACCAAGTCAGTGTGTTCTACAGAAACAGACAAGTTAA  
CAAGTGAACATAATAGAGAGCCAGAAAACAGACCCATCCATTTGGATTGTCACTG  
GAAAGAAGTAGCTTGCAAAACCTTGGAAAAGGAGAGTGTGTGCAATAGATGATGTCG

(SEQ ID NO:90)

33883 TAAAGAAGACTCAGTATAGAAAAGATGTACCTCTCCAAATTGGTGTAGAGATTCAA  
TGCCATTAAAAAAACCCACCTGGTTTTTGGAACTGTCAAGCTGAGTCTCAAATT  
ATATCAAAGAGGCAAAGGCCATAAGAATATCAGGACATTCTGAAGAACTGTAAGGAGCCA  
GGGGCCTGCCCTATCAGATACCAAGGGTTGTATTAGGCATAACCAAGTCAGTGCTGTT  
TCTACAGAAACAGACAAGTTAACAAAGTGAACATAATAGAGAGGCCAGAAACAGACCCAT  
[C,A]  
CATATTTGGATTGTACGTGAAAGAAGTAGCTTGCAAAACTTGGAAAAGGGAGGT  
GTGTGCAATAGATGATGCTCGTGTATGCAGACAAAAAGGAAATTGGGATACCTGCC  
TTACCGTACACAAAACCCAACCTAAACGTGAAAGTTAAACTATAACAGCTTGAGGTGGT  
GGGAAGAAATATCTTATCTCAGTGTAGGGAAAGAATTATTAAAAGAAGACACAAAA  
GGCCATACATAGGAATGAAAAGATTGAATTCAAGCTGCATTAAAAAGATTAAATTCAAGCTG

(SEQ ID NO:91)

34373 TATCTTATCTCAGTGAGGAAGAATTATTTAAAAAGAACACAAAAGGCCATACA  
TAGGAATGAAAAGATTGAAATTCTAGCTGCATTTAAAGATTAAATTCTAGCTGCGTTAAAT  
CAAGAGCATCTGACTTGGACAGCATAGCTGGAAAGACAAAGAGAAGGTATTTGCCAGC  
TTATAACTTGAAGGATTAGAATGAATGATATAAAAGAACTATGTAATAAGAAAAAGACAT

ACAACCGTTAGAAAAACGGGCAAAGACATGAACAGCATATTACACGTGAAGGAAACAGC  
[G,A]  
GTAGCAAATGAACATGGTAAGAGATGCTAACACGTTAGTAATTGAAGGAAATGCAA  
GTTATACCCACAGCAAGACTATCTTATCTAGGAAGTTGTCATAACCTAAATGTTCTGT  
GGTTTTAAGCTACAGAGTTGTAATTCAATTATTCAATAAAACTCAGTGGCAGGC  
ACTGTTTAAAGAACCTTGGTTATAACTTGAATGAAATTAAAAAAATCCTGCCTTGTG  
GAGGATGCTTATGTGTGGGAGTTGGTGGTCAAACAACAATTACATTAAATAG  
(SEQ ID NO:92)

34558 ACTTGAAGGATTAGAATGAATGATATAAAGAACTATGTAATAAGAAAAAGACATACAAC  
CGGTTAGAAAAACGGGCAAAGACATGAACAGCATATTACACGTGAAGGAAACAGCGGTAG  
CAAATGAACATGGTAAGAGATGCTAACACGTTAGTAATTGAAGGAAATGCAAGTTA  
TACCCACAGCAAGACTATCTTATCTAGGAAGTTGTCATAACCTAAATGTTCTGTGGTT  
TTAAGCTACAGAGTTGTAATTCAATTATTCAATAAAACTCAGTGGCAGGCAGTG  
[G,T]  
TTTAGAAACCTTGGTTATAACTTGAATGAAATTAAAAAAATCCTGCCTTGTGGAGGA  
TGCTTATGTGTGGGAGTTGGTGGTCAAACACAATTACATTAAATAGAAAAT  
AGTACATAAAATAACCTATAAAATTGCAACCCAGAGTTATATTAAATGTAAGTAGT  
GACTAGGAACTCTCATGCAGATAACCTCTGTGGTGGACAAATGAAAGTTAAGTGAAT  
TTCCCATATGCAAGTCAAATAAAAGTGCAGACTAGAAAACACAATAATGAATATCTGAA  
(SEQ ID NO:93)

43929 GGCATTTAAGTATTCTGCCATAGGAAGTGTAAAAGTTGAGGCTTTACTTTTATAGG  
TACTATATTGTCCTAAATAATCTCAGCACCTCATGGTGTCAAGGATCTGTGCTTGT  
GGTCAGATTATGTTTATCTCTGCCTAAGGCACCTAACAAATTCTTAAAGGTTACAGA  
ATCTTTTGCCTCATCTGTTAGCATTCAACAGTTGTTGTTCCACAAACTTCAA  
TTTGATTGTTCTTAAATATTCTGCATACTGATGTAACCAAGTTCTATTATTGTGAA  
[T,A]  
CTGCTCCTGAAACCTTAGGAACCTCTGAAGGAGTTTATTATTGTTGTT  
TTGTTTTGTTGTTGTTGAGACGGAGTCTGCTCTGTTGCCAGGCTAGAGTGCAG  
TGGTGCAGCTCGGTCTCTGCAAACCTGCCCTCGGGGTTACGCCATTCTCTGCCTC  
AGCCACCGGAGTAGCTGGACTACAGGCACCCACACTGCCCTGGCTAATT  
ATTTTGTAGAGACGGGTTTCCCGTGTAGCCAGGATGGTCTGATCTCTGACCTT  
(SEQ ID NO:94)

44309 TTGAGACGGAGTCTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGCAGTCGGCTCTC  
TGCAAACCTGGCTCCGGGTTACGCCATTCTCTGCCTCAGCCACCGGAGTAGCTGG  
ACTACAGGCACCCACCACTGCCCTGGCTAATT  
TTTACCGTGTAGCCAGGATGGTCTGATCTCTGACCTTGTAAATCCGCCCCGCTCGCC  
TCCAAAGTGTGGATTACAGGCGTGAGCCACTGTGCCGGCTTTTTTTTTTT  
[T,-,C]  
TTTATGGCTTGTCTTACACTTCAGATTGACTAAATTAAATGCAATTAAATGAAAGT  
CAGGAGTTCACATTGCACTAGAACATGCTAACGTTACATAAAGCATTAAAAATTG  
TTGGTGTAGTGTGCTCTCAGCTATGAGTAAAGATAATTAACTAGTAGTTAGTCTG  
GCCTAGATAAAATTGTACACTATGTGAAGTTATTACATAATTCTACGGTATT  
AGGTAGTTGATAACAGTTGAGACTACAATTGATCTCCATTATTGATAGTAAATGAA  
(SEQ ID NO:95)

44997 GAATTGTAATAATTATTATAGAATTGTTCTCTCAAACCTATAGTAATGTAGAATAGGT  
TGAAGGGGTGATGTTGAAACAATACCTCTCCATTAGCTAAATTATATAGAATCTAT  
TGCATGTTAAATGATAAGTCAGATTATAAAATATTATAAACAGTAGGAAATGA  
GTTTAGGGTATTACACATACAGTTTAATTATTACATATTAAACATATCATGGT  
ATAAAATGATGTGGATATAATTGAGATAAAAGGAAGTATTGTTAAGAATTGATGAAC  
[T,G]  
AATTCTTAAAGATGTCATCACCAAGTTGGTTCTAGCCTTATGAAAATGGTTGCAAT  
AAAAAGATTGACTATGATAAAATGCTGCCCTTCTATTAAACCTAGACCAAGAGAAAAC  
ATACTGTGAATCTATGATGAATGAAAGAAGTTGTAACGTGGTTGTATATTGTA  
TTACTGTTATTCTTCTGTGAACGTGACTGTACTTGTCTTGTGAGTAGACA  
ACTTATAATCTATGACTCAAATTGGTTAGTATAAAATTCTAGGAAATGAAAGTTCATATT  
(SEQ ID NO:96)

46538 TGTTATAACTTATGGTCAACACTTTTATATTGCTGTAGATTCTGTACAAAAAGATTG  
TGACACTGTTAAGCCAGCACTCCCTCAGAATGTACCCAAATCTCAAAATTATTAGG

GGCAAAGCTAATGCTTAAAGAAAAAGGAGA  
[A, G]  
GGGATTGGTGTGTCTTTCTTAGGAACAGTAGTAACCTGACTTTAGAGAACTTGAAT  
AAGCATTATTTTCTCTTGTCTTATTATTGTGAAGTTATTATTTAAAATAAAAT  
GGATTTCTCTGGAATTAGTTCTGCAAATTGAGGAGTTCCAAAGTCAACCTCAGGT  
TTGATACTTCTCTAGAAAGACTCACATAACTCACTGAAAGCTTATTACCCCTGGTTATGG  
TTTATTACGGGAAAAGATGCGGATGAAAATCAAGTAAAGAAGCACATAGGGCAGA

(SEQ ID NO:97)

48153 TTATATCATTCTGCTTTATTTAGGTTACGGTTAAAATCAGACAAAATGAACATAT  
TTGGTGGCTTCGACAGATGGTAAAAGAAGGGAGGTATCCGCTCGTTGGAGGGAAATG  
GTACAAACGTCAAAATTGCTCCTGAGACAGCTGTTAAATTCTGGGATATGAACAGG  
TAATTGTTATCACCGTGGATTAAACAAAGAGGAGTTAGTAAACGGATCAATAAA  
TGTTAATGTATAATGCTTTGGATTCTGTTAATACATGATAATCTTACATATAAC  
[T, C]  
CCATAAGGAGGATCACTTATAGGAGATTAGACTAAATAAAATCAGAGATTCTCATGACC  
AAGTTATGGGATTCTTAATTCTCATATTATTATAAAGTTTTTTCTAAGTAGTT  
TTAAAGGAAGGGTAAATTAGTTATTCTGAATCCTGAGCAGAAGCAGCACACT  
AACATAAGTTTATGAAAGTGTCAAACTCAACCTCTGGAAGGAAACTATAAGTTGAAG  
TCCTTGTGTAATTGACGTTGCTGAAAATTGAGCTGAGTTGGAGTGACACCTCCATG

(SEQ ID NO:98)

48288 AAATTGCTCTGAGACAGCTGTTAAATTCTGGGATATGAACAGTAATTGTTATCACCC  
GTGGAATTTATTAAACAAAGAGGAGTTAGTAAACGGATTCAATAATGTTAATGTATAATG  
CTTTGGGATTCTGTTTAATACATGATAATCTTACATATAACCCATAAGGAGGATC  
ACTTATAGGAGATTAGACTAAATAAAATCAGAGATTCTCATGACCAAGTTATGGGATTC  
TTAATTCTCATATTATTATAAAGTTTTTTCTAAGTAGTTCTAAAGGAAGGGTA  
[G, T]  
AATTTAGTTATTCTGAATCCTGAGCAGAAGCAGCACACTAACATAAGTTTATG  
AAAGTGTACAATCTAACCTCTGGAAGGAAACTATAAGTTGAAGTCCTTGTGTAATT  
GACGTTGCTGAAAATTGAGCTGAGTTGGAGTGACACCTCCATGAAGGCAGGGCGTGG  
CTTCTCCCCATGTACTCCAGCACCTAGACAGAGCTGGCATGTGATAAGTTCAAGCAGTGT  
GTGTCACAATCTAACCTCTGGAAGGAAACTATAAGTTGAAGTCCTTGTGTAATTGAC  
GTGTTGAATGAGTCATGAATGAACAAATGCAATTACCTCTGAATCACTTCTGTGCGC

(SEQ ID NO:99)

48412 TGGGATTCTGTTTAATACATGATAATCTTACATATAACCCATAAGGAGGATCACTT  
ATAGGAGATTAGACTAAATAAAATCAGAGATTCTCATGACCAAGTTATGGGATTCTAA  
TTCATCATATTATTATAAAGTTTTTTCTAAGTAGTTCTAAAGGAAGGGTAAAGT  
TTAGTTTATTCTGAATCCTGAGCAGAAGCAGCACACTAACATAAGTTTATGAAA  
GTGTACAATCTAACCTCTGGAAGGAAACTATAAGTTGAAGTCCTTGTGTAATTGAC  
[G, A]  
TTGCTGAAAATTGAGCTGAGTTGGAGTGACACCTCCATGAAGGCAGGGCGTGGCTTC  
TTCCCCATGTACTCCAGCACCTAGACAGAGCTGGCATGTGATAAGTTCAAGCAGTGT  
TGAATGAGTCATGAATGAACAAATGCAATTACCTCTGAATCACTTCTGTGCGCTTT  
GTAACTGGATTATTGAGCTATTGCTTCAGCCTAACTCAATGTAAGGGAAATACAG  
AGGTAAAGTTAGAGTTGGGTTCTCTTATGGTCATTAGCAGAACTGCTAGTTGAGCA

(SEQ ID NO:100)

48446 CATATACCCATAAGGAGGATCACTTATAGGAGATTAGACTAAATAAAATCAGAGATTTC  
TCATGACCAAGTTATGGGATTCTTAATTCTCATATTATTATAAAGTTTTTTCTA  
AGTAGTTCTAAAGGAAGGGTAAATTAGTTATTCTGAATCCTGAGCAGAAC  
AGCACACTAACATAAGTTTATGAAAGTGTCAAACTCAACCTCTGGAAGGAAACTATA  
AGTTGAAGTCCTTGTGTAATTGACGTTGCTGAAAATTGAGCTGAGTTGGAGTGACA  
[C, G]  
CTCCATGAAGGCAGGGCGTGGCTTCTCCCATGTACTCCAGCACCTAGACAGAGCTTG  
GCATGTGATAAGTTCAAGCAGTGTTGAATGAGTCATGAATGAACAAATGCAATTAC  
TCTGAATCACTTCTGTGCGCTTTGTTAACTGGATTATTGAGCTATTGCTTCAGCC  
TAACTCAATGTAAGGGAAATACAGAGGTAAAGTTAGAGTTGGGTTCTCTTATGGT  
CATTAGCAGAACTGCTAGTTGAGCAGCCACAGATTGTTCCATTATTATCCATC

(SEQ ID NO:101)

48456 ATAAGGAGGATCACTTATAGGAGATTAGACTAAATAAAATCAGAGATTCTCATGACCAA  
GTTATGGGATTCTTAATTCTCATATTATTATAAAGTTTTTTCTAAGTAGTTCTT

AAAGGAAGGGTAGAATTAGTTATTCTGAATCCTGAGCAGAACGACACTAA  
CATAGTTTATGAAAGTGTACAATCTAACCTCTGAGGAAAACATAAGTTGAAGTC  
CTTGTGTAATTGACGTTGCTGAAAATTGAGCTGAGTTGGAGTGCACCTCCATGAA  
[G, C]  
GCAGGGGCGTGGCTTCTCCCCATGTACTCCAGCACCTAGACAGAGCTGGCATGTGATA  
AGTTCAAGCGAGTGTGAATGAGTCATGAATGAACAAATGCATTACCTCTGAATCAC  
TTCTCTGCGCTTTGTTAACCTGGATTATTGAGCTATTGCTCAGCTAACTCAATG  
TAAAGGGAAATACAGAGGTAAGTTAGAGTTGGGTTCTCTTATGGTCATTAGCAGA  
ACTGTCTAGTTGAGCAGCCACAGATTATGTTCCATTATTATCCATCATTGTTATC

(SEQ ID NO:102)

48789 GCACCTAGACAGAGCTGGCATGTGATAAGTTCAAGCGAGTGTGAATGAGTCATGAA  
TGAACAAATGCATTACCTCTGAATCACTCTCTGCGCTTTGTTAACCTGGATTATT  
TGAGCTATTGCTCAGCTAACTCAATGAAAGGGAAATACAGAGGTAAGTTAGAGT  
TTGGGTTCTCTTATGGTCATTAGCAGAACTGTCTAGTTGAGCAGCCACAGATTATGTT  
TCCATTATTATTCATCATTGTTATCAAGGACTGTAAGGGCTGAAATTCACTCCC  
[C, -]  
CCCCCATAGTTTGTATTATTCCATGTAGATTAGATTATTCTGGAGAGTGTGTTGTT  
CTTGAGCAACAGAAACTCTTGAGAAGATTACGAAGTCCAGTGGTATCCTTTCTTGCC  
TAGGAAATAGAGAAGCAAAAAAAAAAAAAAAATTAAAGAAAATCTAGTCTCCAGG  
ATTTAATTAGAACCTATCTGGGAAGGCTATTCTCTTATATGAAGGTTGAAGATT  
AAATCATGATTATAAGGGCTAATGTTGAGATACCCCTAGGTTATTCTGACCACATACT

(SEQ ID NO:103)

48859 CATTACCTCTGAATCACTCTGCGCTTTGTTAACCTGGATTATTGAGCTATTG  
CTTCAGCCTAACTCAATGAAAGGGAAATACAGAGGTAAGTTAGAGTTGGGTTCTC  
TTTATGGCATTAGCAGAACTGTCTAGTTGAGCAGCCACAGATTATGTTCCATTATT  
ATTCCATCATTGTTATCAAGGACTGTAAGGGCTGAAATTCAACTCCCCCCCCCATAG  
TTTTGTTATTCCATGTAGATTAGATTATTCTGGAGAGTGTGTTGTTGAGCAA  
[G, C]  
AGAATACTCTTGAGAAGATTACGAAGTCCAGTGGTATCCTTTCTTGCTAGGAAATAG  
AGAAGCAAAAAAAAAAAAAAAATTAAAGAAAATCTAGTCTCCAGGATTAAATT  
GAACCTATCCTGGGAAGGCTATTCTCTTATATGAAGGTTGAAGATTCAAATCATGAT  
TATTAAGGGCTAATGTTGAGATACCCCTAGGTTATTCTGACCACATACTGGATT  
GATAGGAAAGCCACAGCCTAAAATAAAACTCAATGCAGTTATTCACTGAGAAG

(SEQ ID NO:104)

49126 GATTATTCTGGAGAGTGTGTTCTGAGCAACAGAACACTCTTGAGAAGATTACGAAG  
TCCAGTGGTATCCTTCTTGCTAGGAAATAGAGAAGCAAAAAAAAAAAAAAA  
ATTAAGAAAATCTAGTCTCCAGGATTAAATTAGAACCTATCCTGGGAAGGCTATT  
CCTTATATGAAGGTTGAAGATTCAAATCATGATTATTAGGGCTAATGTTGAGATACC  
CTTAGGTTATTCTGACCACATACTGGATTATGATAGGAAAGCCACAGCCTAAAATA  
[A, G]  
TAAATACTCAATGCAGTTATTCTAGTATGCAAGAAGTTGGTATTGAAAAAGTCAT  
GGGTATTGCAAGCAAATATGCACATTGCTTATGCCATTGTCAGATTCTACCTTG  
ATACCACCAACAGGCATCCTCTGCTCTGCCACCCAGCTCCCTGAGACCTCTT  
TAGTATTGTAATTCTGCACACTAACTTCTTAGACATGAAGAGAAAGCTGCTACACAG  
TGTGGTGTAGTTCTTATGGGCTCTGGACCTATGGTGTGTTCTCTCCTGCTGA

(SEQ ID NO:105)

49378 TGACCACATACTGGATTATGATAGGAAAGCCACAGCCTAAAATAAAACTCAA  
TGCAGTTATTCTAGTATGCAAGAAGTTGGTATTGAAAAAGTCATGGGTATTGCAA  
GCAAATATGCACATTGCTTATGCCATTGTCAGATTCTACCTGGATACCACCAAC  
AGGCATCCTCTGCTCTGCCACCCAGCTCCCTGAGACCTCTTATAGTATTGTA  
TTCTGACACTAACTTCTTAGACATGAAGAGAAAGCTGCTACACAGTGTGGTGTAGT  
[T, G]  
TTCTTATGGGCTCTGGACCTATGGTGTGTTCTCTCCTCTGCTGAAGGTCCATT  
CCCTCGGGCTCTCTAAAGCCACCTCCCTGTGACAAGCATATAACTAAGCATCTCAATCA  
AAGCCAGTCTCCCTGTCCAGCCTCCCTGAGTGTGAGATTGAGAATATCCATT  
TCATTGGATGATGGAAAACCCATTGTTCCAGTGGATTGAAATTACTCAGGGTAA  
TAGGCTGTATATATTCTCAAATTCCAGAGTATGTAACTAGGTCACTTGTAGATT  
CAGA

(SEQ ID NO:106)

49482 TCCATGGTATTGCAAGCAAATATGCACATTGGCTTATGCCATTGGTAGATTCTTAC  
CTTGGATACCAACAGGCATCCTCTGCTTCTGCAACCCAAAGCTCCCTGAGACCT  
CTTATAGTATTGTATTCTGACACTAACTTCTTAGACATGAAGAGAAAGCTGTCTA  
CACAGTGGGTAGTTCTATGGGCTGGACCTATGGTCTGTTCTCCCT  
GCTGAAGGTCCATTATCCCTGGGCTCTAAAGCCACCTTCTGTGACAAGCATAT  
[A, C]  
CTAAGCATCTCAATCAAAGCCAGTTCTCCCTGTCAGCCTCCCTGAGTGTGAATTG  
AGAATATCCCATTTCATTGGATGATGAAAACCCATTGTTTCCCAGTGGATTGTA  
ATTACTTCGGGTAATAGGCTGTATATATTCTAAATTCCCAGAGTATGTAACTAGGT  
CACTTTAGATTAGATAGATTGTCTGAATAGCTAGTACTTTAGGAAACTAAGAA  
AAAGATCTTCAACCTGGTATGTAGCTGTCAAACACATCATCAGTATGGGAAACC (SEQ ID NO:107)

49741 CTCGGGCTCTAAAGCCACCTCCCTGACAAGCATATACTAAGCATCTCAATCAA  
GCCAGTTCTCCCTGTCAGCCTCCCTGAGTGTGAATTGAGAATATCCCATTTC  
ATTGGATGAGGAAAACCCATTGTTCCCAGTGGATTGAAATTACTCGGGGAAATA  
GGCTGTATATATTCTAAATTCCCAGAGTATGTAACTAGGTACTTTAGATTAGATA  
GATTTGTTCTGAATAGCTAGTACTTTAGGAAACTAAGAAAAGATCTTCAACCTG  
[G, A]  
TATGTAGCTCTGTCAAACACATCATCAGTATGGGTAACCTGTGTTCTGTGGGTTGT  
CATTACCATAGTAGTGTCAATTGTATCATTGACAGTGTAAAGTGTGGGTTAGTGTCTG  
TGGTTCACTGCCCCACTCTGTACTGACTGCTTCCACTCCA (SEQ ID NO:108)

49840 ATCTTTCAACCTGGTATGTAGCTCTGTCAAACACATCATCAGTATGGGTAACCTGTG  
TTCTGTGGGTTGTCAATTACCATAGTAGTGTCAATTGTATCATTGACAGTGTAA  
[A, G]  
TAGTGTGGGTTAGTGTCTGTGGGTTCAAGCTGCCACTCTGTACTGACTGCTTCCACTC  
CAACATCTCTCTTATCTAAACACTGTAGGTCTACCTGTACTGTGTGTTCACTG  
CTCTGCTTGATGACCCAGGAGTGCCTCCACTCAATATGCCACCATGATGGTATCT  
TTCTGCTACTCCCTGCTCTGACCCCTGCTCAGCAACACAGACAGACACCCCTCT  
TCTATATGTATGGTGGGAAATGCCTTAGTACTTACTCAGGAGTTAGTCTCTG (SEQ ID NO:109)

50102 CATTACCATAGTAGTGTCAATTGTATCATTGACAGTGTAAAGTGTGGGTTAGTGTCTG  
TGGTTCACTGCCACTCTGTACTGACTGCTTCCACTCCAACATCTCTCTTTATCTC  
AAACACTGTAGGTCTACCTGTACTGTGTTCAAGCTCTGCTTGATGACCCAGGA  
GTGCCTCCACTCAATATGCCACCATGATGGTATCTCTGCTACTCCCTGCTCT  
GACCCCTGCTCCAGCAACACAGACAGACACCCCTCTTCTATATGTATGGTGGG  
[G, A]  
ATGCCCTTACTTACTCAGGAGTTAGTCTCTGGGAAGCCCTCTGTTAGTTCTAGTTCC  
TTTGTACAGCACTTACATTGAATTCTGACGTTCTGTACTTATCTGTTGTGAG  
ACTGTGAGCTTCTTAGGCAGTAGTACTTGTATTCTGACCTTGCCAGTGCAGGA  
AACCTTATTAAGTAAATGAAAGACAGAACTGACAGACTGAAATTAGAGCTAAGCTT  
CCTCAATCTCAAGCATTAAAGATGAAGGGAGCCGGCGTGGTGGCTACGCCCTAATC (SEQ ID NO:110)

50109 ATAGTAGTGTCAATTGTATCATTGACAGTGTAAAGTGTGGGTTAGTGTCTGTGGTTTC  
AGCTGCCACTCTGTACTGACTGCTTCCACTCCAACATCTCTCTTTATCTCAACACTG  
TAGGTCTACCTGTACTGTGTTCAAGCATCTCTGCTTGATGCCAGGAGTGCCTC  
CCACTCAATATGCCACCATGATGGTATCTCTGCTACTCCCTGCTCTGACCCCTG  
CTCCAGCAACACAGACAGACACCCCTCTTCTATATGTATGGTGGGAAATGCC  
[C, G, T]  
TTAGTACTTACTCAGGAGTTAGTCTCTGGGAAGCCCTCTGTTAGTTCTTGTGTT  
ACAGCACTTACATTGAATTCTGACGTTCTGTACTTATCTGTTGTGAGACTGTGA  
GCTTCTTAGGCAGTAGTACTTGTATTCTGACCTTGCCAGTGCAGGAAACCTT  
ATTAAGTAAATGAAAGACAGAACTGACAGACTGAAATTAGAGCTAAGCTTGCCTCAAT  
CTCAAGCCATTAAAGATGAAGGGAGCCGGCGTGGTGGCTACGCCCTAATCCAGCAC (SEQ ID NO:111)

50747 CCAGCCTGGCAACGTGGAAAACCCATTCTACAAAAAATATAAAATTAGTGGACG  
TGGGGTGTGCTGTACTCAGGATGCTGAGGTGGGAGGATCACTGAGCTGAGAGGC  
AGAGGTTGAGCTGGGATCACACCATTGCAATCTAGCCTGGTGTAGAATGAGAC

CTTGTCTCAAAAAAAATAAATAAAATAAAAGGGGAAGATAAGGATTGAAACAGAA  
GGAGCAGCATGTGGACAGAAATGTAGGCACAAGAAGGCATCACTCACTGAAGAGACTGAA  
[G,A].  
GTGGTTCACTGTGCCCTAAGACTGGTGGAGTGTGTTCCGGAAAGATAATGATGAAAGAG  
CTGGACAGATAAACAGGGGCAAATGTAATAGGAGTCTGGATTATTCTGAATATGGTA  
GGGGCTATTGTAGCATTTATAGGGAAAGTGAATAGTACATTACATTAAAGGAATA  
TCAACCTGAAAAAAGAGTGGAGACATTGTTGGGGAGAGTGGAGGTAGACTAGAGGCAGGG  
AGAATATTAAATAATTGAGGTAGAAAATGATGAACACCACTATAAGGTGATGTTAA

(SEQ ID NO:112)

51272 TAGACTAGAGGCAGGGAGAATTTAAATAATTGAGGTAAGAAATGATGAACACCACTAT  
AAGGTGATGTCCTTAAGGAATGGAGAAGGAACTGAACTGAGAAATTTGGAAAGTAGAA  
TCAACAGAACTCACTGACTGACTGGATATGGAGGTGAGAAAGAGAAGAGTCAGAAATGAT  
ATTCTAATTCTAACCTGAGTGAATGACTGCATTCAAAGAGAATACAATATCAGGTTCCATT  
GTGCATGCTGAGTTGAGATGTGTGGGACATGTACAGGGAGCTGTCCAGTAAGCAATTGG  
[G,A]  
TATATCAGCTAGCCATTAAAGAGAGAGATCTTGATAGAGAGGTTGTGCTGAGTTGAGCC  
ATTGGAATGGCAGGATCACTCAAGAAGAGCTTATAATGAGAAGAATTCTAGGAATAAG  
TCCAAAGGGAGAAGTAAAAGAAGAAACTTGCAAAGGACACTGAGAAGAAATAGCTCGAGG  
GATGGGAGAAATCCAGAGAGAGGGATGGCATAGGAGTCAGTGGAGGAAACCGTTTCA  
GGGGTCACTACTGGTAGTGAATATAAGAATATCTTTAGGATTTCTCAACCC

(SEQ ID NO:113).

52842 TCAGGGTGGTTTGAGGGCTCAGTTAAGTCTCTTCTAGGAAGGTCAGTTCTGTAGCCCTGGCAAGTTACTTAAAGTCTGTGACTATTACCTATCTCTAAGATGGGACTAAGCTTGTGACATAGTTTACATACCAAGGCACAGTGCTGACTTTTGCTCTGTCTGAAGTCTTCCCTTGTATATGGTATGTTGGGGAAATAGGAGCCTCAAGCACTTATCTTTAAATATTATCCTCCATCAGTCACTAAACGTTACTCTGTACTTTGATAGGTGCTGTGGGGTCCA  
[G,A] GGTATAAAAGGTACCTTCAAAGTTACTGTTAAAGTGCAGGAAGGTTTAAGCAAATTATGTTAATGATTTGACAATCTGACATGCAGGAAAATTAAATAGGGCTATGCAGAAGAGGA  
GTTTATGTAACACTCTGTAGTTAGGAAACAGAGCCCTGGAAGCAGTGATCTCTGGGGAGGAATGTCGGTATTTGGGAATCTCATGAAATGATAATATACTTAAATTATCATGAGCAGCAAAACACAGATTGCTAGGAGAAAGTCATCGTATGTTGCTTGGCACTTT

(SEQ ID NO:114)

(SEQ ID NO:115)

62018 CATATTTAGGAGCTTAATATTAGGCCATATGAAGTTATAATTCTTCCTGGTAAAGT  
GACCATTATCATTATGTAATGCCATCTTGTCTTGTGACAGTTGTGCTTTAAAA  
TCTATTTGTCTGATGTAATTATGGCCACCCCTTTCTCTTGGGTTCCGGTTTATGG  
AATATCTTTCCATCCTTCACTTCAGCTTATGTGTGCTTAGATCTAAAGTGAGTC  
TCATAGATAAGGTATAGTTGATTCTGTATGTGTTATTCACTCAGCAATTATATCTTTA  
[A, G].  
TTAGGGATTTAATCCATTACATTAAAGCAGTTACTGATAAGGAAGGACTTACTGTTG  
TCATTGGCTAGCTACCTTTATCTTGTCTGTGGCTTTCTGTTTCCCTTCCCT  
CTTCCCTGGCTTCTCTGTGTTTGTGATTTTTTTTGTAGTGTATGTTCTGAT  
TCCCTTCTCATTTCCCTTGTGTGCAATTCTATAGATGCTATTGGGTTACCAATTGCA  
ACTACATAAAAGCATACTAAAGTTATAGCAACTTATTAAAGCTGTTACAACCTAACCTC

(SEQ ID

65562 GACTGAAATTAGACACATGCACTGATTCTAACCTCTGTGCCAGCTGATCCA  
GAACCTTGATGACTGATACTGGCTGATAGATTGTCTATGGCTGATAGACTGTCATTTCTG  
ACCTAAAGTCTGATCATTACATCTGTTAGACATCTTGAGCCTTCGGTGTCACT  
TCCAAAGTTGTTAGTGGAAATTCAAAGCCTTAATAATCTAGCCCCACTTGTCACTC  
TCTGTGATAAACACATACAACAATTGGCTGATCTCCATAGCACATGGTACTCTCCC  
[A, G]  
TTGTCTTGGTTGTGCCAGCAACACTGGTTTCGTTCTCTCCGTGTTGGTGGAGGTCA  
TTCCAAGGCCAGGTCTTGTGCTTTTCCAAGCTCCAGAGCTTCCATACTCCC  
CTTACTTCTGAGATTTAACTGTTCTCTCAGCGCTGTCTAGTAAGAAGGAGGCAGC  
AGCAGCACTGTGGGTGGTGGAAAGTGTACCGAGCTTGGAGTCAGACCATTGGATCTAG  
CCCTACCATTCTACTTAGATTTTTAGGACAAATTCTCCATCTTCTAAGCCTCCA

(SEQ ID NO:117)

65780 TCTAGCCCCACTTGTCACTCTGTGTAATAACCACATACAACAATTGGCTGCACTCTC  
CATAGCACATGGTACTCCTCCCGTTGCTTGGTTGTGCCAGCAACACTGGTTTCGCTTT  
CTCTTCTGCTTGTTGAGGTCAATTCCAAGGCCAGGTCTTGTGCTTTTCCCAAGCTT  
CCCAGAGCTTCCATACTCCCCCTACTTCTGAGATTTAACTGTTCTCTCTCAGCGC  
TTGTCTAGTAAGAAGGAGGCAGCAGCACTGTGGGGTGGTGGAAAGTGTACCGCTTT  
[G, A]  
GAGTCAGACCATTGGATCTAGCCCTACCATTCTACTTAGATTTTTAGGACAAATT  
TCTCCATTTCTAAGCCTCCAATTGCTCACTTACAAAATTGATATAACATTACCTTG  
AAGATTGGTATGGAAGGTAAATTAAACCCAGTATTAGAACATAGTAATTAAATAAACTA  
TTATTACCATCATTACTATAGTTAGGACACTCACTGTAGGTCTATACAAAGAGGATCA  
TAAAGGGATGTTGCTTGGGCTCTTGAATAAAATGTTGCTTTACTGTATTITAGA

(SEQ ID NO:118)

66092 TTGGATCTAGCCCTACCATTCTACTTAGATTTTTAGGACAAATTCTCCATCTT  
CTAACGCCTCAATTGCTCACTTACAAAATTGATATAACATTACCTTGCAAGATTGGTAT  
GGAGGTAAATTAAACCCAGTATTAGAACATAGTAATTAAATAAACTATTACCATC  
ATTACTATAGTTAGGACACTCACTGTAGGTCTATACAAAGAGGATCATAAAAGGGATG  
TTGTCTTGGCTTCTTGAATAAAATGTTGCTTTACTGTATTAGAATATCATTCTG  
[G, A]  
GTCATAATTGTTGTTGTCATAATAATGAAACATACTTGAATATTAAATTACCTCTTT  
TTTATTTTTAGCCATGTTAGAAGGTTCCCACAGCTGAATATGTTGGCCTTTGAC  
GAATTATTTCAAAGAAGGAATACCAGGACTTACAGAGGCATCACCCCAAACITCATGA  
AGGTGCTCCCTGCTGTAGGCATCAGTTATGTGGTTATGAAAATATGAAGCAAACCTT  
GAGTAACCCAGAAATGATGTTGCACTTGTGCTTACGCTGATAATTGAAACATTCAACA

(SEQ ID NO:119)

66617 ATGAAGCAAACCTTGGAGTAACCCAGAAATGATGTTGCACTTGTGTTAGCCTGATA  
ATTGAAACTTCACAATCTGGAGTGAATTCTCCCTCGAATTGAAACAAGTCTATG  
GCAAAAGAGCTGCACTTCTACAAAAGGGAGATGGTAACAATGGTCACCTCAAAC  
TTGGGCTAAATTATATGTACACAGAAATGTTCAAATCATAGTTTAATGTGTTGAA  
AAGGCCACACAATTACTTATCTTCTTAATAATCCTGCAAATCTGCCCTGAATC  
[C, T]  
GAAATCTGAAAATGTAAGGCTGAAACAAAATTGTTGTTGTTAGAGTTATAAATCA  
TTAATCTTATTTCGGGTGGTTACGTTATGCCAGTTCTTATATTAAATTCTTGT  
TTTATATTTGAATGTTAGATTCTTAAATTCTTATAGAACCTTAAAGTATAGGGTTA  
AAAATCATTACATTAAATACCTTACAGCAAAGCATCCAATAAGTATAGGGTTA  
TGTCTTATTCTTCTTCAAGCTGAATACGAATGAGCACAGTGGTGGAAATTCTGAAGGG  
[G, A]

(SEQ ID NO:120)

66892 ATCCTGCAAATCTCTGCCCTGAATCCGAAATCTGAAAATGTAAGGCTGAAACAAAATT  
GTTTGTGTTAGAGTTATAAATCATTAAATCTTATTCTGGGGGGTTACGTTATGCC  
AGTTCCCTTATATTAAATTCTGTTATATATTGTAATGTTAGATTCTT  
AAATTCTTATAGAACCTTAAATAGAAAATCATTACATTAAATACCTTACAGCAA  
AAGCATCCAATAAGTATAGGGTTATGTCCTTATTCTTCTTCAAGCTGAATACGAATGA  
[G, A]  
CACAGTGGTGGAAATTCTGAAGGGAGTGATGAAATTATATTCTAGTGGGCACTTT  
TCCATTCTTACACTGTACCAATTCTTGGTCTGGAGTTACACACTAATTCTCAGTATAT  
TACTGTTAAATTACCAACACAAGGCAATTATTGAAAGATTCCGTTATCTGCCATTG  
CTTGAAAAGCAGCAGGAAACGAAATCCTTACTGTATCAGCTCTGAGAGCATCTT

TGTTTTCTTTGCTTTGTTCTTACCTTTGAATCAGATTCGTTTAGTCAGGAAGA (SEQ ID NO:121)

67263 . CACTGTACCATTATTTGGTTCCTGGAGTTATACACTAATTTCAAGTATATTACTGTAAAG  
TTACCAACACAAGGCAATTATTTGAAAGATTCCGTTTATCTGCCATTGCTTGAAAG  
CAGCAGGAAACGAAATCCTTGTACTTGATCAGCTTCTGCAGAGCATCTTGTCTTCCCTT  
TGTCTTGTCTTCTCACCTTGTAACTCAGATTCCGTTTACTCAGGAAGACTCTGGGA  
CCATTCTTAGTAACCTGAAATTCTTTTAATTGCATGAAGTGGATTGATCATGAGCAA  
[G,A].  
TGATGTGCTTATTCCTCCCTCACTGTGAATATCTTGAATTGCTGTCTTCAATATGGG  
CAGCACAAGGTGAGAGATAACATATTAAATAGTAGTATGTATTACTCTTATACATTAGATA  
CCTATATTTAAATGAAAGGCCAATTGTAAACATATACATTCAATTCTCTTGCCTT  
AAGTTTGTAGGAACATGTAGGATATAGGAGACTTAATTATAATAATGAGAGCATT  
TATTCTACTAAAGCCATTATAGTCACATCTTCTTATTGTGTTGATTAGAACTT

(SEQ ID NO:122)

67651 ATAGTAGTATGTATTACTCTTATACATTAGATACTATATTTAAATGAAAGGCCAACTT  
GTAACATATACTACATTCTATTCCTCTGGCCCAAGTTTAGGAACATGTTAGGATATAG  
GAGACTTAATTATAATAATGAGAGCATTTTATTTACTAAAGCCATTATAGTC  
AACTATCTTTCTTATTTGTGTGATTAGAACCTAGAAAAATATTACTAGTTGAAGTTAT  
TATCAGTTTAATTAGTCTTAAACTCATTCTACTCTAAATAATTCTGTTATAAATT  
[G, T]  
CCAGCATTAAATGAAAATCTAATGATGTAATAGGCATTTCTTATTGAAACCTACCTC  
TTTATTCTGAACCAAAGAGAAAGATGGACTGGTGTGAAACATTAAAAATG  
TAGTTTCATTATATTAGTTATGTTGATAAAATGTCTCAGTATTTTATAATATGATAAG  
CCTGGGATTCTACTTTAGGGTTATTGTACTTTGAGTAATATATAAAGTGACAATT  
AAGGTACATGATCAGCTTTCTATTCTACTCGAAAAATTATGGAAATGAATAATT

(SEQ ID NO:123)

67935 ATTTCTGTATAAAATTGCCAGCATTTAATGAAAATCTAATGATGTAATAGGCATTTCT  
TTATTTGAACTTACCTCTTTTATTTCTGAACCAAGAGAAAGATGGACTGGTGTGTTG  
AAACATTTTAAAATGTAGTTCTATTATATTAGTTATGTTGATAATGTCAGTAT  
TTTTATAATATGATAAGCCTGGGATTCTACTTTAGGGTTATTTGACTTTGAGTAATA  
TATAAAGTGACAATATTAAAGGTACATGATCAGCTCTTCTATTTTACTCGTAAAAATT  
[C, T]  
GGAAATGAATAATTGCTAACAACTTGAATTCAGGAAATATGAAAATA  
TTCATTGTTCATATTGAATTAAATTGTAAGGTATGAATGTGATTGTCGTACATCTG  
TATCTTTCCAAAAATGATTCTGTATCTTGGAAAAAGCCGAGAGTTGAAGATAGTA  
TATTCTGGTAGTACTGAATATTACTACAGTTCTATCAAAATATATATTGTTCT  
AAAATTACTTGTTCAGTTTATTAGAGAAAATTCTAAGTCTCAGTTCC

(SEQ ID NO:124)

69000 TTCAGAAATAACTTATCAGTTATTCGTAGCTTCTGCTTACCTGGATACCTGACAGG  
TGAGATGGCTGTAGCAGACACTGGCAGTTCCTGCCACACACCTGTCCTGTCCACAGC  
TGCACAAGGCAGCTCTGTGTGCAATTGCCAGCATCTGCTCTGTCTCAGGGAATCTT  
TGTTAGAAAAATGCTGCCATATTGTTCTCACCTATTAGCTTGTCTCCAGTCAGAG  
AATAAATTATGCAAGCAGAGATTGTACTTACAGTATTGTCTTGAAGCTTGGCATT  
[T,G]  
GTTGCCATTGTAAAAATGTGGCATGGCTTCCTCATCCCCCAATAGGAACCTTGCCAGCCC  
TTTGTTCTCATGGAACCTCCCTTTGAAAAGAGCACCAAGGAGTAAAAAATCTGTGG  
AGGGAGCAACCCCTCCCTGGCATATGCTCTCATGGGAGACATGTGGAGCAGTCTGAAGT  
CATTTAGGCCACTCTCTGGGAGAGCACATCCTATGATGTTCTCCAGCCTAGCCCCCTCC  
ACTGTGCTCAAGTCAAGCTGACCAGCTTCTGACCACAGTGTAAACAAGATGATTGTC

(SEQ ID NO:125)

69134 CTGTGTGCAATTGCCAGCATCTGCTCCCTGTTCTCAGGGAATCTTGTAGAAAAATGC  
TGCCATATTGTTCTCACCTATTAGTCTTGTCTCCAGTCAGAGAATAAAATTATGCA  
AGCAGAGATTGACTTTACAGTATTTGTCTTGAGCTGGCATTAGGTGCAATTGAA  
AAATGTGGCATGGCTTCTCATCCCCCAATAGGAACCTTGCCAGCCCTTTGTTCTCATG  
GAACCTCCTTTTGAAAAGAGCACCAAAGGAGTAAAAACTGTGGAGGGAGCAACCT  
[C, T]  
CTTGGCCATATGCTCTCATTGGGAGACATGTGGAGCAGTCTGAAGTCATTAGGCCACTC  
TCTGGGAGAGCACATCCTATGATGTTCTCCAGCTAGCCCCCTCCACTGTGCTCAAGTC

## FIGURE 3SS

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Serial No.: To Be Assigned

Inventors: Gennady MERKULOV et al.

Title: ISOLATED HUMAN TRANSPORTER ...

CAAGCTGACCAGCTTCTGACCACAGTGAAACAAAGATGATTGTCAGTGGCCCCAGAA  
TCCTATACCCAGA (SEQ ID NO:126)

FIGURE 3TT